

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 14:13:59 ; Search time 1420 Seconds
(without alignments)
32.939 Million cell updates/sec

Title: US-10-006-190-1

Perfect score: 1161

Sequence: 1 MGASARLRRAVIMGAPGSGK.....VYAFIQTKVPQRSQKASYTP 227

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

SPTREMBL_21:*

- 1: sp.archaea:*
- 2: sp.bacteria:*
- 3: sp.fungi:*
- 4: sp.human:*
- 5: sp.invertebrate:*
- 6: sp.mammal:*
- 7: sp.mhc:*
- 8: sp.organelle:*
- 9: sp.phage:*
- 10: sp.plant:*
- 11: sp.todent:*
- 12: sp.virus:*
- 13: sp.vertibrate:*
- 14: sp.unclassified:*
- 15: sp.virus:*
- 16: sp.bacteriap:*
- 17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1156	99.6	227	4 Q9NPB4	Q9NPB4 h cDNA flj1
2	1078	92.9	227	4 Q9D721	Q9D721 mus musculu
3	1074	92.5	227	11 Q9DBM5	Q9DBM5 mus musculu
4	1073	92.4	227	11 Q9DBS7	Q9DBS7 mus musculu
5	1054	90.8	227	6 Q9S394	Q9S394 oryctolagus
6	899	77.4	189	11 Q9D8W6	Q9D8W6 mus musculu
7	809	69.7	157	4 Q9HC01	Q9HC01 homo sapien
8	698	60.1	136	4 Q9H576	Q9H576 homo sapien
9	565	48.7	216	5 Q9VG06	Q9VG06 drosophila
10	439	37.8	248	10 Q9EK35	Q9EK35 arabidopsis
11	438	37.7	221	16 Q8R7X4	Q8R7X4 thelmoanar
12	433.5	37.3	231	3 Q9S985	Q9S985 neocallimas
13	424	36.5	231	3 Q9S987	Q9S987 piromyces s
14	413	35.6	232	11 Q9CY37	Q9CY37 mus musculu
15	411	35.4	232	3 Q9S986	Q9S986 neocallimas
16	399	34.4	209	10 Q9MAY0	Q9MAY0 oryza sativ

17	398.5	34.3	240	5 Q9U915	Q9U915 drosophila
18	393	33.9	220	5 Q9Y0A8	Q9Y0A8 cryptospori
19	385.5	33.2	215	17 Q8TR53	Q8TR53 mechanosarc
20	378	32.6	237	5 Q9W1D0	Q9W1D0 drosophila
21	365	31.4	202	4 Q8TCY3	Q8TCY3 homo sapien
22	364.5	31.4	159	2 Q9G011	Q9G011 haemophilus
23	364	31.4	159	2 Q9G0D4	Q9G0D4 haemophilus
24	364	31.4	159	2 Q9G0C4	Q9G0C4 haemophilus
25	364	31.4	159	2 Q9G0I2	Q9G0I2 haemophilus
26	364	31.4	159	2 Q9AM09	Q9AM09 haemophilus
27	362.5	31.2	220	17 Q8U207	Q8U207 pyrococcus
28	360	31.0	159	2 Q9G0C7	Q9G0C7 haemophilus
29	358.5	30.9	211	16 Q8RE31	Q8RE31 fusobacteri
30	329.5	28.4	588	10 Q8VYX1	Q8VYX1 arabidopsis
31	323	27.8	155	2 Q9R452	Q9R452 neisseria m
32	323	27.8	155	2 Q9R452	Q9R452 neisseria m
33	322	27.7	155	2 Q9R452	Q9R452 neisseria m
34	321	27.6	155	2 Q9R452	Q9R452 neisseria m
35	319.5	27.5	217	10 Q9FY07	Q9FY07 arabidopsis
36	319	27.5	283	10 Q9FY07	Q9FY07 arabidopsis
37	315	27.1	155	2 Q9R452	Q9R452 neisseria m
38	305	26.3	149	3 Q9G6V01	Q9G6V01 neocallimas
39	303	26.1	149	3 Q9G6V02	Q9G6V02 piromyces s
40	294.5	25.4	151	3 Q9G6V00	Q9G6V00 neocallimas
41	292.5	25.2	269	5 Q9G9I0	Q9G9I0 leishmania
42	280	24.1	229	5 Q9Y0E7	Q9Y0E7 leishmania
43	278.5	24.0	196	16 Q8UE38	Q8UE38 agrobacteri
44	271	23.3	284	10 Q9ZU01	Q9ZU01 arabidopsis
45	268	23.1	130	4 Q8TCY2	Q8TCY2 homo sapien

ALIGNMENTS

RESULT 1

Q9NPB4 PRELIMINARY: PRT: 227 AA.

AC Q9NPB4: 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE CDNA FLJ11089 fis, clone PLACE1005305, highly similar to GTP:AMP

DE phosphotransferase mitochondrial (EC 2.7.4.10) (CDNA FLJ10691 fis,

DE clone NT2RP3000359, highly similar to GTP:AMP phosphotransferase

DE mitochondrial) (CDNA FLJ14628 fis, clone NT2RP2000379, highly similar

DE to GTP:AMP phosphotransferase mitochondrial) (Hypothetical 25.6 kDa

DE protein).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

ON [1]

RP SEQUENCE FROM N.A.

RC TISSUE=PLACENTA;

RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

RA Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,

RA Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,

RA Nakamura Y., Nagahari K., Masuno Y., Sasaki N.,

RA "NEO human cDNA sequencing project."

RA Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

RL [2]

RP SEQUENCE FROM N.A.

RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

RA Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K.,

RA Tanai H., Kimata M., Watanabe M., Hirooka S., Ishii S., Kawai Y.,

RA Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K.,

RA Masuno Y., Kanehori K.,

RA "NEO human cDNA sequencing project."

RA Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

RL [3]

RP SEQUENCE FROM N.A.

RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,

RA Wagatsuma M., Hosoliri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takenashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
 RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagehara K., Masuno Y.,
 RA Niimiya K., Iwayanagi T.,
 RT "NEO human cDNA sequencing project."
 RN Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
 [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LYMPH;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1 SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
 DR EMBL; AK001951; BAA91996.1; -;
 DR EMBL; AK001553; BAA91753.1; -;
 DR EMBL; AK027534; BAB55183.1; -;
 DR EMBL; BC013771; AAH13771.1; -;
 DR HSSP; P08760; 2AK3.
 DR InterPro; IPR000850; Adenylate_kin.
 DR InterPro; IPR000623; Shik_kinase.
 DR Pfam; PF00406; adenylatekinase; 1.
 DR PRINTS; PR00094; ADENYLTKINASE.
 DR PRINTS; PR01100; SHIKIMTKINASE.
 DR Prodom; PD00657; Adenylate_kin; 1.
 DR PROSITE; PS00113; ADENYLATE_KINASE; 1.
 KW Hypothetical protein; kinase; transferase.
 SQ SEQUENCE 227 AA; 25565 MW; 98A0EDFAFD9C9CEF CRC64;

Query Match 99.6%; Score 1156; DB 4; Length 227;
 Best Local Similarity 99.1%; Pred. No. 3,1e-94;
 Matches 225; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGASARLLRAVIMGAPGSGKGVSSRITTHFEFLKHLSSGDLRDNMRLRGTETGVLAKAFI 60
 DB 1 MGASARLLRAVIMGAPGSGKGVSSRITTHFEFLKHLSSGDLRDNMRLRGTETGVLAKAFI 60
 QY 61 DQGLIIPDDVMTRLALHELKNTLTQYSWLIDGFPRTLPOAEALDRAYQIDVTINLVNPFV 120
 DB 61 DQGLIIPDDVMTRLALHELKNTLTQYSWLIDGFPRTLPOAEALDRAYQIDVTINLVNPFV 120
 QY 121 IKQRLTARWIHPASGRVNIIEFNPPKTVGIDDLTGEPILQREDDPETVYIKRLKAYEQT 180
 DB 121 IKQRLTARWIHPASGRVNIIEFNPPKTVGIDDLTGEPILQREDDPETVYIKRLKAYEQT 180
 QY 181 KXVLXYQKGVLETFSGTETNKIMPYVAFLOTQVPPQSRQASVTP 227
 DB 181 KPVLEYQKGVLETFSGTETNKIMPYVAFLOTQVPPQSRQASVTP 227

RESULT 2

QY 09D721 PRELIMINARY; PRT; 227 AA.
 AC Q9D721;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Adenylate kinase 3 alpha like.
 GN AKJ3L.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID-10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6J; TISSUE-STOMACH;
 RX MEDLINE-21085660; PubMed-11217851.
 RA Kawai J., Shunagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aikawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H. A., Ashburner M., Batalov S., Casavant T.,
 RA Fletschmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Mashio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,
 RA Wyszynski B., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection."
 RN Nature 409:685-690(2001).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-COLON;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1 SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
 DR EMBL; BC016432; AAH16432.1; -;
 DR EMBL; BC019174; AAH19174.1; -;
 DR EMBL; BC024871; AAH24871.1; -;
 DR HSSP; P08760; 2AK3.
 DR MGD; MGI:1860835; AKJ3L.
 DR InterPro; IPR000850; Adenylate_kin.
 DR InterPro; IPR000623; Shik_kinase.
 DR Pfam; PF00406; adenylatekinase; 1.
 DR PRINTS; PR00094; ADENYLTKINASE.
 DR PRINTS; PR01100; SHIKIMTKINASE.
 DR Prodom; PD00657; Adenylate_kin; 1.
 DR PROSITE; PS00113; ADENYLATE_KINASE; 1.
 KW kinase; transferase.
 SQ SEQUENCE 227 AA; 25426 MW; 6601DE10971DE5AC CRC64;

Query Match 92.9%; Score 1078; DB 11; Length 227;
 Best Local Similarity 92.1%; Pred. No. 2.4e-87;
 Matches 209; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1 MGASARLLRAVIMGAPGSGKGVSSRITTHFEFLKHLSSGDLRDNMRLRGTETGVLAKAFI 60
 DB 1 MGASARLLRAVIMGAPGSGKGVSSRITTHFEFLKHLSSGDLRDNMRLRGTETGVLAKAFI 60
 QY 61 DQGLIIPDDVMTRLALHELKNTLTQYSWLIDGFPRTLPOAEALDRAYQIDVTINLVNPFV 120
 DB 61 DQGLIIPDDVMTRLALHELKNTLTQYSWLIDGFPRTLPOAEALDRAYQIDVTINLVNPFV 120
 QY 121 IKQRLTARWIHPASGRVNIIEFNPPKTVGIDDLTGEPILQREDDPETVYIKRLKAYEQT 180
 DB 121 IKQRLTARWIHPASGRVNIIEFNPPKTVGIDDLTGEPILQREDDPETVYIKRLKAYEQT 180
 QY 181 KXVLXYQKGVLETFSGTETNKIMPYVAFLOTQVPPQSRQASVTP 227
 DB 181 EPNLYQKGVLETFSGTETNKIMPHYVAFLOTQVPPQSRQASVTP 227

RESULT 3

QY 09DBM5 PRELIMINARY; PRT; 227 AA.
 AC Q9DBM5;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Adenylate kinase 3 alpha like.
 GN AKJ3L.

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=LIVER;
RX MEDLINE=21085660; Pubmed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilmink L.,
RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
DR EMBL: AK004864; BAB23625.1; -;
DR HSSP: P08760; 2AK3.
DR MGD: MGI:1860835; AK131.
DR InterPro: IPR000850; Adenylate_kin.
DR InterPro: IPR000623; Shik_kinase.
DR Pfam: PF00406; adenylatekinase; 1.
DR PRINTS: PR00094; ADENYLTKINASE.
DR PRINTS: PR01100; SHIKMTKINASE.
DR ProDom: PD000657; Adenylate_kin; 1.
DR PROSITE: PS00113; ADENYLATE_KINASE; 1.
KW kinase; transferase.
SQ SEQUENCE 227 AA; 25427 MW; 680FDF1E9J1DE5AC CRC64;

Query Match 92.5%; Score 1074; DB 11; Length 227;
Best Local Similarity 91.6%; Pred. No. 5.4e-87;
Matches 208; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 1 MGASARLLRAVINGAPSGKGTSSRTTTHFEKLKHLSSGDLRLDNLGTEIGYLAKAFI 60
Db 1 MGASGRLLRAVINGAPSGKGTSSRTTKHPELKLHSSGDLRLQNLGTEIGYLAKTFI 60

QY 61 DQGLIPDDVWTRIALHELKNLTQYSWLDGFPPTLPQAEALDRAYIDIVININVPFV 120
Db 61 DQGLIPDDVWTRIALHELKNLTQCSWLDGFPPTLPQAEALDRAYIDIVININVPFV 120

QY 121 IKORLTARWHPASGRYNIENFPKPTVGIDDLGEPFLIOEDDKPETVIRLKAAYEDQ 180
Db 121 IKORLTARWHPASGRYNIENFPKPTVGIDDLGEPFLIOEDDKPETVIRLKAAYEDQ 180

QY 181 KXVLXYQKKGVLTFESGTEETNKIMPYVYAFLOTKVPQRSOKASVTP 227
Db 181 EPVLQYQKKGVLTFESGTEETNKIMPYVYAFLOTKVPQRSOKASVTP 227

RESULT 4
Q9DB57
ID 09DB57 PRELIMINARY; PRT; 227 AA.
AC 09DB57;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Adenylate kinase 3 alpha like.
GN AKL3L.
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=CEREBELLUM;
RX MEDLINE=21085660; Pubmed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilmink L.,
RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
DR EMBL: AK005194; BAB23876.1; -;
DR HSSP: P08760; 2AK3.
DR MGD: MGI:1860835; AK131.
DR InterPro: IPR000850; Adenylate_kin.
DR InterPro: IPR000623; Shik_kinase.
DR Pfam: PF00406; adenylatekinase; 1.
DR PRINTS: PR00094; ADENYLTKINASE.
DR PRINTS: PR01100; SHIKMTKINASE.
DR ProDom: PD000657; Adenylate_kin; 1.
DR PROSITE: PS00113; ADENYLATE_KINASE; 1.
KW kinase; transferase.
SQ SEQUENCE 227 AA; 25427 MW; 660B7FBA971DE5AC CRC64;

Query Match 92.4%; Score 1073; DB 11; Length 227;
Best Local Similarity 91.6%; Pred. No. 6.6e-87;
Matches 208; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 1 MGASARLLRAVINGAPSGKGTSSRTTTHFEKLKHLSSGDLRLDNLGTEIGYLAKAFI 60
Db 1 MGASGRLLRAVINGAPSGKGTSSRTTKHPELKLHSSGDLRLQNLGTEIGYLAKTFI 60

QY 61 DQGLIPDDVWTRIALHELKNLTQYSWLDGFPPTLPQAEALDRAYIDIVININVPFV 120
Db 61 DQGLIPDDVWTRIALHELKNLTQCSWLDGFPPTLPQAEALDRAYIDIVININVPFV 120

QY 121 IKORLTARWHPASGRYNIENFPKPTVGIDDLGEPFLIOEDDKPETVIRLKAAYEDQ 180
Db 121 IKORLTARWHPASGRYNIENFPKPTVGIDDLGEPFLIOEDDKPETVIRLKAAYEDQ 180

QY 181 KXVLXYQKKGVLTFESGTEETNKIMPYVYAFLOTKVPQRSOKASVTP 227
Db 181 EPVLQYQKKGVLTFESGTEETNKIMPYVYAFLOTKVPQRSOKASVTP 227

RESULT 5
Q95J94
ID 095J94 PRELIMINARY; PRT; 227 AA.
AC 095J94;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Adenylate kinase 3.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-RENAL PROXIMAL TUBULE;
RX MEDLINE=2140235; PubMed=11342145;
RA Brochiero E., Coady M.J., Klein H., Laprade R., Laporte J.Y.;
RT "Activation of an ATP-dependent K(+) conductance in Xenopus oocytes by
RT expression of adenylate kinase cloned from renal proximal tubules.";
RL Blochm. Biophys. Acta 1510:29-42(2001).
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
DR EMBL: AF41508; AL07503.1; -
DR Interpro: IPR000850; Adenylate_kin.
DR Pfam: PF00406; adenylatekinase.1.
DR Prodom: PD000657; Adenylate_kin.1.
DR PROSITE: PS00113; ADENYLATE_KINASE; UNKNOWN.1.
KW Kinase; Transferase.
SQ SEQUENCE 227 AA; 25610 MW; ECDDIDFA89228A4E CRC64;

Query Match 90.8%; Score 1054; DB 6; Length 227;
Best Local Similarity 91.2%; Pred. No.3.2e-85;
Matches 207; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY 1 MGASARLLRAVINGAPGSGKGVSSRTTHFEELKHLSSGDLRDNLRGTEIGVLAKAFI 60
DB 1 MGASGRLLRAVINGAPGSGKGVSSRTTHFEELKHLSSGDLRQNMRLGTEIGVLAKFTI 60
QY 61 DQGLIPDDVMTLALHELNLTQYSWLDGFPRTLPQALDRAYOIDTVINLVNPFV 120
DB 61 DQGLIPDDVMTLALHELNLTQYSWLDGFPRTLPQALDRAYOIDTVINLVNPFV 120
QY 121 IKORLTARWTHPASGRVYNIENFPKPTVGIDLTGEPLIOREDDEKPEYIKRLKAYEDQ 180
DB 121 IKORLTARWTHPASGRVYNIENFPKPTVGIDLTGEPLIOREDDEKPEYIKRLKAYEDQ 180
QY 181 KAVLXYQKGVLEFSGETNKIMPYVAFIQTKVPSQKASVTP 227
DB 181 EPVLEYRKGVLEFSGETNKIRPNVYAFIQTKIPEAHQKDSVTP 227

RESULT 6
Q9D8W6 PRELIMINARY; PRT; 189 AA.
AC Q9D8W6;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE 10 day old male pancreas cDNA, RIKEN full-length enriched library,
DE clone:1810027K10, full insert sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE-PANCREAS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shigaawa A., Shibata K., Yoshino M., Toh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai R., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bernaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Guentlich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Norioka P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schenbach C., Seiya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohlsuki S.,

RA Hayashizaki Y.;
RT "functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
DR EMBL: AK007618; BAB25139.1; -
DR HSSP: P08760; 2AK3.
DR Interpro: IPR000850; Adenylate_kin.
DR Interpro: IPR000623; Shik_kinase.
DR Pfam: PF00406; adenylatekinase.1.
DR PRINTS: PR00094; ADENYLTKINASE.
DR PRINTS: PR01100; SHIKMTKINASE.
DR Prodom: PD000657; Adenylate_kin.1.
DR PROSITE: PS00113; ADENYLATE_KINASE; 1.
KW Kinase; Transferase.
SQ SEQUENCE 189 AA; 21193 MW; 822ADB21804F5336 CRC64;

Query Match 77.4%; Score 899; DB 11; Length 189;
Best Local Similarity 93.1%; Pred. No.1.2e-71;
Matches 176; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 MGASARLLRAVINGAPGSGKGVSSRTTHFEELKHLSSGDLRDNLRGTEIGVLAKAFI 60
DB 1 MGASGRLLRAVINGAPGSGKGVSSRTTHFEELKHLSSGDLRQNMRLGTEIGVLAKFTI 60
QY 61 DQGLIPDDVMTLALHELNLTQYSWLDGFPRTLPQALDRAYOIDTVINLVNPFV 120
DB 61 DQGLIPDDVMTLALHELNLTQYSWLDGFPRTLPQALDRAYOIDTVINLVNPFV 120
QY 121 IKORLTARWTHPASGRVYNIENFPKPTVGIDLTGEPLIOREDDEKPEYIKRLKAYEDQ 180
DB 121 IKORLTARWTHPASGRVYNIENFPKPTVGIDLTGEPLIOREDDEKPEYIKRLKAYEDQ 180
QY 181 KAVLXYQK 189
DB 181 EPVLEYQYQK 189

RESULT 7
Q9HC01 PRELIMINARY; PRT; 157 AA.
AC Q9HC01;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE GTP:AMP phosphotransferase.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PHEOCHROMOCYTOMA;
RA Li Y., Peng Y., Jiang Z., Gu W., Han Z., Chen Z.;
RT "A novel gene expressed in human pheochromocytoma.";
RT Submitted (SEP-1999) to the EMBL/Genbank/DBD databases.
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
DR EMBL: AF183419; AAG09688.1; -
DR HSSP: P08760; 2AK3.
DR Interpro: IPR000850; Adenylate_kin.
DR Pfam: PF00406; adenylatekinase.1.
DR PRINTS: PR00094; ADENYLTKINASE.
DR Prodom: PD000657; Adenylate_kin.1.
DR PROSITE: PS00113; ADENYLATE_KINASE; 1.
KW Kinase; Transferase.
SQ SEQUENCE 157 AA; 18192 MW; F7D36803A8A21A4 CRC64;

Query Match 69.7%; Score 809; DB 4; Length 157;
Best Local Similarity 98.7%; Pred. No.8.4e-64;
Matches 155; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 71 MTRLALHELNLTQYSWLDGFPRTLPQALDRAYOIDTVINLVNPFVIKORLTARWI 130
DB 1 MTRLALHELNLTQYSWLDGFPRTLPQALDRAYOIDTVINLVNPFVIKORLTARWI 60

Query Match	Best Local Similarity	Score	DB	Length
Matches 96; Conservative 42.3%; Mismatches 41; Indels 6; Gaps 2;	Matches 85; Conservative 42; Mismatches 67; Indels 6; Gaps 2;	37.7%; Score 438; Pred. No. 8e-31;	DB 16;	Length 231;
37.3%; Score 433.5; DB 3; Length 231;	42.3%; Pred. No. 2.1e-30;			
Matches 96; Conservative 41; Mismatches 81; Indels 9; Gaps 3;				

DE	01-MAR-2002 (TReMBLrel. 20, last annotation update)
DR	Adenylylate kinase (EC 2.7.4.3) (Fragment).
GN	HDCAK12.2
OS	Neocallimastix frontalis (Rumen fungus).
OC	Eukaryota; Fungi; Chytridiomycota; Neocallimasticales;
OC	Neocallimastixaceae; Neocallimastix.
OX	NCBI_TaxID=4757;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=L2;
RA	Voncken F., Boxma B., Verhagen E., van Wesel R., van der Drift C.,
RA	Veehuis M., Hackstein J., Vogels G.;
RT	"Evidence for a chimeric origin of chytrid hydnosomes."
RL	Submitted (FEB-1998) to the EMBL/Genbank/DBD databases.
CC	-1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
CC	EMBL: AJ224659; CAA12056.1; -.
DR	HSSP; P07170.1AKY.
DR	InterPro: IPR000850; Adenylylate_kin.
DR	Pfam: PF00406; adenylylatekinase.1.
DR	PRINTS; PR00094; ADENYLTKINASE.
DR	ProDom: PD000657; Adenylylate_kin.1.
DR	PROSITE: PS00113; ADENYLATE_KINASE; 1.
KW	kinase; transferase.
FT	NON_TER 232
SO	SEQUENCE 232 AA; 25441 MW; 1B74EPD7C97891F2 CRC64;
Query Match	35.4%; Score 411; DB 3; Length 232;
Best Local Similarity	41.4%; Pred. No. 2,1e-28;
Matches	94; Conservative 38; Mismatches 73; Indels 22; Gaps
OY	4 SARLLRAVINGAPSGSGKGVSSRTITTHPELKLHSSGDLRLDNMLKRGTEIGVLAFAFDG 63
DB	6 SKNSLRVMVYPPGSGSKGTQAPKVYCDYCIChLADGMLRAVYKAGTPIGMAKKIMDG 65
OY	64 KLIPDVMTRALHNL-----KNLTQYSMLDGFPRTLPLQAAALD-----RAYQIDTYN 113
DB	66 GLVSEIIVYNLIKELMDTRACKN---GFILDGFPRTYAQAOKLDBMLEQRNOKLDTLAE 121
OY	114 LNVPEVITKQRLTARMIHPASGRVYNIIEFN-PKTVGIDDLGEPFLIOREDKPEVIR 172
DB	122 LTVDSLLFKRTITGRLVHPASGRSYHKITFNPNQKVEGKDDITGEPFLIQSDSTEAALKR 181
OY	173 LKAYEDQKXYLVXYOKKGVLETFSGTEFNK-----IWPYVAFLOTK 215
DB	182 LVYHKKQTVPAVDYKKKKGI--KGVGVAQDPAAVVMQMQAFIESEK 225

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Search completed: March 19, 2003, 16:32:44
Job time : 1423 secs
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GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 15:24:06 ; Search time 690 seconds
(without alignments)
31.627 Million cell updates/sec

Title: US-10-006-190-1

Perfect score: 1161

Sequence: 1 MGASARLLRAVIMGAPGSGK.....VYAFLOTQVPOBSQKASVTP 227

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 segs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1091	89.4	227	2 A34442	nucleoside-triphos
2	1038	89.4	227	2 JQ1945	nucleoside-triphos
3	700.5	60.3	223	1 K1H0A3	adenylate kinase
4	447.5	38.5	214	2 I64062	adenylate kinase
5	439.5	37.9	225	2 S23568	adenylate kinase
6	437	37.6	217	2 T44404	adenylate kinase
7	436	37.6	220	2 S31338	adenylate kinase
8	435	37.5	222	1 K1BYA	adenylate kinase
9	431	37.1	222	2 JC5893	adenylate kinase
10	431	37.1	229	2 G02248	adenylate kinase
11	430	37.0	215	2 S61841	adenylate kinase
12	430	37.0	215	2 F81154	adenylate kinase
13	428	36.9	218	2 S43016	adenylate kinase
14	425	36.6	215	2 S61843	adenylate kinase
15	424	36.5	215	2 G83184	adenylate kinase
16	419	36.1	224	2 B29792	adenylate kinase
17	417	36.1	241	2 JS0422	adenylate kinase
18	417	35.9	215	2 H90019	adenylate kinase
19	417	35.9	215	2 AB1777	adenylate kinase
20	416	35.8	248	2 S44765	adenylate kinase
21	415	35.7	229	2 JQ1944	adenylate kinase
22	413	35.6	214	2 AC0563	adenylate kinase
23	408	35.1	215	2 AC1401	adenylate kinase
24	407	35.1	215	2 H97282	adenylate kinase
25	405	34.9	214	1 K1E0CA	adenylate kinase
26	405	34.9	214	2 C85545	adenylate kinase
27	405	34.9	214	2 G90694	adenylate kinase
28	401.5	34.6	214	2 C82255	adenylate kinase
29	401	34.5	217	2 JS0492	adenylate kinase

30	400	34.5	214	2 AG0378	adenylate kinase
31	395.5	34.1	217	2 D69334	adenylate kinase
32	395	34.0	222	2 T27960	adenylate kinase
33	393	33.9	206	2 G70307	adenylate kinase
34	389	33.5	199	2 PC4230	adenylate kinase
35	383.5	33.0	214	2 S70734	adenylate kinase
36	375	32.3	212	2 B95027	adenylate kinase
37	374	32.2	212	2 B97898	adenylate kinase
38	366.5	31.6	215	2 E84986	adenylate kinase
39	365.5	31.5	205	2 S50007	adenylate kinase
40	364	31.4	217	1 K1BSAF	adenylate kinase
41	355.5	30.6	220	2 G72247	adenylate kinase
42	352.5	30.4	220	2 F71052	adenylate kinase
43	346	29.8	215	2 E86884	adenylate kinase
44	343	29.5	220	2 E75090	adenylate kinase
45	340	29.3	215	2 S17987	adenylate kinase

ALIGNMENTS

RESULT 1

A34442

nucleoside-triphosphate-adenylate kinase (EC 2.7.4.10) 3, mitochondrial - bovine

N;Alternate names: adenylate kinase 3

C;Species: Bos primigenius taurus (cattle)

C;Date: 15-Jun-1990 #sequence, revision 15-Jun-1990 #text, change 03-Jun-2002

C;Accession: A34442; JH0512; A24201

R;Yamada, M.; Shahjahan, M.; Tanabe, T.; Kishl, F.; Nakazawa, A.

J. Biol. Chem. 264, 19192-19199, 1989

A;Title: Cloning and characterization of cDNA for mitochondrial GTP:AMP phosphotrans

A;Reference number: A34442; MUID:90037053; PMID:2478555

A;Accession: A34442

A;Molecule type: mRNA

A;Residues: 1-227 <YAM>

A;Cross-references: GB:M25757; NID:g163527; PIDN:AAA30705.1; PID:g163528

R;Shahjahan, M.; Yamada, M.; Tanaka, H.; Nakazawa, A.

Gene 107, 313-317, 1991

A;Title: Cloning and characterization of the gene encoding bovine mitochondrial adeny

A;Reference number: JH0512; MUID:92084124; PMID:11748300

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-50 <SHM>

R;Romasselli, A.G.; Frank, R.; Schlitz, E.

FEBS Lett. 202, 303-308, 1986

A;Title: The complete primary structure of GTP:AMP phosphotransferase from beef heart

A;Reference number: A24201; MUID:86248102; PMID:3013690

A;Accession: A24201

A;Molecule type: protein

A;Residues: 2-10, 12-227 <TOM>

C;Genetics:

A;Gene: AK3

A;Intons: 51/1; 91/1; 148/3; 188/2

C;Superfamily: adenylate kinase

F;2-227/Product: GTP-AMP phosphotransferase, mitochondrial #status predicted <MAT>

F;14-21/Region: nucleotide-binding motif A (P-loop)

Query Match 94.0%; Score 1091; DB 2; Length 227;

Best Local Similarity 91.6%; Pred. No. 5.8e-05;

Matches 208; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY	1	MGASARLLRAVIMGAPGSGKTVSSRTTTHFELKHLSSGDLRDNMLRGTEIGYAKAFI	60
DB	1	MGASARLLRAVIMGAPGSGKTVSSRTTTHFELKHLSSGDLRDNMLRGTEIGYAKAFI	60
QY	61	DGGLIPDDVWTRALVLEHLKLNLYSWLDGFPPTLQAEALDAVYIDPYNINLVPEV	120
DB	61	DGGLIPDDVWTRALVLEHLKLNLYSWLDGFPPTLQAEALDAVYIDPYNINLVPEV	120
QY	121	IKORLTARWTHPASGRYVNIENFPKTVGIDDLGEPFLIOREDDEPTVIKRLAYEDQT	180
DB	121	IKORLTARWTHPASGRYVNIENFPKTVGIDDLGEPFLIOREDDEPTVIKRLAYEDQT	180

Db 121 IKORLARMIHPASGRVNIENFNPRTMGIDLTGEPVLQREDDRETYVKRLKAEADQ 180
QY 181 KXVLYXQKGVLETFSGTETNKIMPYVAFLOTQKVPORSOKASVTP 227
Db 181 EPLVLEYRKKGVLETFSGTETNKIMPYVAFLOTQKVPORSOKASVTP 227

RESULT 2

Query Match 89.4%; Score 1038; DB 2; Length 227;
Best Local Similarity 90.3%; Pred. No. 1.8e-80;
Matches 205; Conservative 6; Mismatches 16; Indels 0; Gaps 0;
Nucleotide-triphosphate-adenylate kinase (EC 2.7.4.10) 3, mitochondrial - rat
N.Alternate names: GTP-AMP phosphotransferase AK3
C.Species: Rattus norvegicus (Norway rat)
C.Date: 03-Feb-1994 #sequence-revision 03-Feb-1994 #text-change 03-Jun-2002
C.Accession: J01945
R.Tanabe, T.; Yamada, M.; Noma, T.; Kajii, T.; Nakazawa, A.
J. Biochem. 113, 200-207, 1993
A.Title: Tissue-specific and developmentally regulated expression of the genes encoding
A.Reference number: P00534; MUID:93224500; PMID:8468325
A.Accession: J01945
A.Molecule type: mRNA
A.Residues: 1-227 <TAN>
C.Cross-references: DDBJ:D13062; NID:g220797; PIDN:BAA02379.1; PID:g450312
C.Superfamily: adenylate kinase
C.Keywords: ATP, GTP, mitochondrion, nucleotide binding, P-loop, phosphotransferase
F:14-21/Region: nucleotide-binding motif A (P-loop)

QY 1 MGASARLRAVIMGAPSGKGVSSRTTHFELKHLSSGDLRDNNLRGTETGLAKAFI 60
Db 1 MGASGRLLRAVIMGAPSGKGVSSRTTHFELKHLSSGDLRDNNLRGTETGLAKAFI 60
QY 61 DOGKLLPDDVMTRLALHEKLNLTQYSWMLDGPRTLPQAEALDRAVDITVINLNPFEV 120
Db 61 DOGKLLPDDVMTRLALHEKLNLTQYSWMLDGPRTLPQAEALDRAVDITVINLNPFEV 120
QY 121 IKORLARMIHPASGRVNIENFNPRTMGIDLTGEPVLQREDDRETYVKRLKAEADQ 180
Db 121 IKORLARMIHPASGRVNIENFNPRTMGIDLTGEPVLQREDDRETYVKRLKAEADQ 180
QY 181 KXVLYXQKGVLETFSGTETNKIMPYVAFLOTQKVPORSOKASVTP 227
Db 181 EPLVLEYRKKGVLETFSGTETNKIMPYVAFLOTQKVPORSOKASVTP 227

RESULT 3

Query Match 89.4%; Score 1038; DB 2; Length 227;
Best Local Similarity 90.3%; Pred. No. 1.8e-80;
Matches 205; Conservative 6; Mismatches 16; Indels 0; Gaps 0;
Nucleotide-triphosphate-adenylate kinase (EC 2.7.4.10) 3 - human
N.Alternate names: adenylylate kinase 3
C.Species: Homo sapiens (man)
C.Date: 17-Apr-1993 #sequence-revision 23-Mar-1995 #text-change 03-Jun-2002
C.Accession: A42820; S16381
R.Xu, G.; O'Connell, P.; Stevens, J.; White, R.
Genomics 13, 537-542, 1992
A.Title: Characterization of human adenylylate kinase 3 (AK3) cDNA and mapping of the AK3
A.Reference number: A42820; MUID:92347846; PMID:1639383
A.Accession: A42820
A.Molecule type: mRNA
A.Residues: 1-223 <XUG>
A.Cross-references: EMBL:X60673; NID:g28576; PIDN:CAA43088.1; PID:g28577; GB:S41502
A.Experimental source: frontal-cortex
A.Note: sequence extracted from NCBI backbone (NCBIN:109644, NCBI:109645)
C.Comment: This isoform is found in the mitochondrial matrix.
C.Genetics:
A.Gene: GDB:AK3
A.Cross-references: GDB:118988; OMIM:103030
A.Map position: 9pter-9p13
C.Function:
A.Description: catalyzes the reversible phosphorylation of adenine monophosphate with nu
C.Superfamily: adenylylate kinase

C.Keywords: ATP, mitochondrial matrix, mitochondrion, P-loop, phosphotransferase
F:12-19/Region: nucleotide-binding motif A (P-loop) #status atypical
F:85-89/Region: nucleotide-binding motif B #status atypical
F:22,33,35,88/Active site: Cys, His, Ser, Asp #status predicted

Query Match 60.3%; Score 700.5; DB 1; Length 223;
Best Local Similarity 58.8%; Pred. No. 6.2e-52;
Matches 130; Conservative 38; Mismatches 52; Indels 1; Gaps 1;

QY 4 SARLLRAVIMGAPSGKGVSSRTTHFELKHLSSGDLRDNNLRGTETGLAKAFIDOG 63
Db 2 ASKLLRAVIMGAPSGKGVSSRTTHFELKHLSSGDLRDNNLRGTETGLAKAFIDOG 61
QY 64 KLIPDDVMTRLALHEKLNLTQYSWMLDGPRTLPQAEALDRAVDITVINLNPFEV 123
Db 62 LVPDVTIRLMSELENRGQHWMLDGPRTLPQAEALDRAVDITVINLNPFEV 121
QY 124 RLTARMIHPASGRVNIENFNPRTMGIDLTGEPVLQREDDRETYVKRLKAEADQ 183
Db 122 RLSRRMIHPASGRVNIENFNPRTMGIDLTGEPVLQREDDRETYVKRLKAEADQ 181
QY 184 LXXYXQKGVLETFSGTETNKIMPYVAFLOTQKVPORSOKASVTP 223
Db 182 IELYSRGVLDHPSGTETNKIMPYVAFLOTQKVPORSOKASVTP 222

RESULT 4

Query Match 38.5%; Score 447.5; DB 2; Length 214;
Best Local Similarity 46.1%; Pred. No. 1.5e-30;
Matches 95; Conservative 37; Mismatches 61; Indels 13; Gaps 4;
Adenylylate kinase (EC 2.7.4.3) - Haemophilus influenzae (strain Rd KW20)
N.Alternate names: ATP-AMP phosphotransferase
C.Species: Haemophilus influenzae
C.Date: 18-Aug-1995 #sequence-revision 18-Aug-1995 #text-change 18-Jun-1999
C.Accession: I64062; S15290
R.Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage
; Goeyne, J.D.; Scott, J.; Shiley, R.; Liu, L.T.; Glodex, A.; Kelley, J.M.; Weidman
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995
A.Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter
A.Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A.Reference number: A64000; MUID:9550630; PMID:7542800
A.Accession: I64062
A.Status: nucleic acid sequence not shown; translation not shown
A.Molecule type: DNA
A.Residues: 1-214 <TIGR>
A.Cross-references: GB:U32719; GB:I42023; NID:g1573310; PIDN:AAC22010.1; PID:g1573319
A.Experimental source: strain Rd KW20
R.Maskell, D.J.; Szabo, M.J.; Butler, P.D.; Williams, A.E.; Moxon, E.R.
Mol. Microbiol. 5, 1013-1022, 1991
A.Title: Molecular analysis of a complex locus from Haemophilus influenzae involved in
A.Reference number: S15287; MUID:92065797; PMID:1956282
A.Accession: S15290
A.Molecule type: DNA
A.Residues: 1-77, 'A', '79-214 <MAS>
A.Cross-references: EMBL:X57315; NID:g43587; PIDN:CAA40570.1; PID:g43591
A.Experimental source: strain RM7004
A.Gene: adh
C.Function:
A.Description: catalyzes reversible phosphorylation of AMP with ATP to form two ADP
C.Superfamily: adenylylate kinase
C.Keywords: ATP, monomer, P-loop, phosphotransferase
F:7-14/Region: nucleotide-binding motif A (P-loop) #status atypical
F:80-85/Region: nucleotide-binding motif B #status atypical
F:30,84/Active site: Ser, Asp #status predicted

QY 8 LRAVIMGAPSGKGVSSRTTHFELKHLSSGDLRDNNLRGTETGLAKAFIDOG 67
Db 1 KRIILGAPGAGGTGTOAFITMKFGIPQISTGDMRAATKAGTELGKAKALMDESKLP 60

```

Oy 68 DD--VMTLALHEKLNLTQYSLWDGFPRLTPQAL-DRAVQIDTVNLNPEFYI 121
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 61 DELVALVAKDKIAQADCTN----GFLDGFPRITLQADALDSGVKIDFLFEDPDEV 116

Oy 122 KQRLTARNIHPSAGRWYIEFNPKPTVGIDDLTGEPLLOREDDKPREYIKRLKAYEDQTK 181
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 117 VERMSGRVHOAGSGRSYHIVNPNPKVEKGDVYTGSDLLITRADDKREYTLDSLAVYHNKQTS 176

Oy 182 XLVLYTQ---KKGVLETFSGTETNKI 204
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 177 PLIDYQAQAKRAGNTQYERLDTQKV 202

RESULT 5
S23568
adenylate kinase (EC 2.7.4.3) ADK2 - yeast (Saccharomyces cerevisiae)
N:Alternate names: PAK3 protein; protein YER170w
C:Species: Saccharomyces cerevisiae
C:Date: 12-Mar-1993 #sequence,revision 12-Mar-1993 #text_change 19-Jan-2001
C:Accession: S23568; JCI135; S50673
R:Schrlicker, R.; Magdolen, V.; Bandlow, W.
MOL. Gen. Genet. 233, 367-371, 1992
A:Title: A new member of the adenylate kinase family in yeast: PAK3 is highly homologous
A:Reference number: S23568; MUID:92318888; PMID:1620094
A:Accession: S23568
A:Molecule type: DNA
A:Residues: 1-225 <SCOH>
A:Cross-references: EMBL:X65126; NID:94096; PIDN:CAA46254.1; PID:94097
R:Cooper, A.J.; Friedberg, E.C.
C:Date: 114, 145-148, 1992
A:Title: A putative second adenylate kinase-encoding gene from the yeast Saccharomyces
A:Reference number: JCI135; MUID:92267376; PMID:1587477
A:Accession: JCI135
A>Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-225 <COO>
A:Cross-references: GB:M7757; NID:g171045; PIDN:AAA34418.1; PID:g171046
R:Dietrich, F.S.
A:Description: The sequence of S. cerevisiae cosmids 9163 and 9132.
A:Reference number: S50673
A:Accession: S50673
A:Molecule type: DNA
A:Residues: 1-225 <DIE>
A:Cross-references: EMBL:U18922; NID:9603405; PIDN:AAB64697.1; PID:9603411; MIPS:YER170w
C:Genetics:
A:Gene: SGD:ADK2; PAK3
A:Cross-references: SGD:S0000972; MIPS:YER170w
A:Map position: 5R
C:Function:
A:Description: phosphotransferase
A:Superfamily: adenylate kinase
C:Keywords: ATP; mitochondrion; nucleotide binding; P-loop; phosphotransferase
C:21-28/Region: nucleotide-binding motif A (P-loop)

Query Match 37.9%; Score 439.5; DB 2; Length 225;
Best Local Similarity 44.9%; Pred. No. 7.6e-30;
Matches 93; Conservative 37; Mismatches 66; Indels 11; Gaps 4;

Oy 8 LRAVIMGAPSGKGTVSSRTTTH-ELKHSSGDLRLDNMLRGTEIGVLAFAFDQGLI 66
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 15 LRLLLGAPGSGKGTQYTRLLKQIPQLSSISSGDLRQEIKESESTLGGREATYIAGKRL 74

Oy 67 PDDVWTRLALHEKNL-----TOYSLWDGFPRLTPQALDRAVQ-----IDTVNLNVP 117
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 75 PDDLTLTRTLTRLSALGLKPSAMWLDGFPRTTAQAASALDELKQHDASINLVVELDP 134

Oy 118 FEVIKQRLTARMIHPASGRVNIIEFNPKPTVGIDDLTGEPLLOREDDKPREYIKRLKAYE 177
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 135 ESTLIERENKYNVHPSGRVNIENLPKPYGDLDTITSEPLTKRLDPAIEVFKRRLRETK 194

Oy 178 DQTKXVLXYQKKGVLTFSGTETNKI 204

```

```

Db      195   KTNEPLKDYKKSGIFGVSG-ETSDI    220
          : ||| | : || | : |
RESULT 6
T44404
adenylate kinase (EC 2.7.4.3) [imported] - Bacillus halodurans
C:Species: Bacillus halodurans
C:date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 15-Jun-2001
C:Accession: T44404; C83669
R:Takami, H.; Takaki, Y.; Nakasone, K.; Hirama, C.; Inoue, A.; Horikoshi, K.
Biosci. Biotechnol. Biochem. 65, 452-455, 1999
A:title: Sequence analysis of a 32-kb region including the major ribosomal protein gene
A:Reference number: 22756; MUID:99209008; PMID:10192328
A:Accession: T44404
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-217 <STO>
A:Cross-references: EMBL:AB017508; NID:94512395; PIDN:BAA75292.1; PID:94512425
C:Experimental source: strain C-125
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A:title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans s
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: C83669
A:Status: preliminary
A:Molecule type: DNA
A:Gene: adk
C:Superfamily: adenylate kinase
C:Keywords: phosphotransferase

Query Match              37.6%; Score 437; DB 2; Length 217;
Best local similarity    42.7%; Pred. No. 1,2e-29;
Matches 85; Conservative 47; Mismatches 61; Indels 6; Gaps 2;

OY      8   LRAVIMGAPSGCKTVSSRTTHFELKLHSSGDLLRDMLNGTEIGVLAKAFIDQKLIIP 67
          : ||| | | | | | : | : | : | : | : | : | : | : | : | : | : | : |
DB      1   NWLILMGIPGAGCKQAQAEKIIEKYGIPIHISTGMDFRAMKNMETELGLAKASYMDAGEIYP 60
          : ||| | | | | | : | : | : | : | : | : | : | : | : | : | : | : |

OY      68   DDVMRLALHET-KNLQYSMLDGFPRTLPOAEALDRAY-----OIDTVNLNWPREVI 121
          : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB      61   DEVTIGIVRDIRLSDDCONCFLDGFPRIVAQAELEILLASLDKRLDYVINIDVPEQL 120
          : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

OY      122  KORLTARWIIHPASGRVNYIEFNPKTWIDDLTGEPFLIQREDDKPETYIKRLKAYEDQT 181
          : ||| | : | | | | : | | | : | : | : | : | : | : | : | : | : | : |
DB      121  MDRLGRRVSPISGRTYHYTFNPFRVEGICVDGSELIQRDDRPETVKRKRLVNQANQAO 180
          : ||| | : | | | | : | | | : | : | : | : | : | : | : | : | : | : |

OY      182  XVLXLYOKKGVLFFSGTE 200
          : : | : | | | : : | :
DB      181  PLIDFYSEKGYLQNINGDO 199
          : : : | : | | : : | :

RESULT 7
S31338
adenylate kinase (EC 2.7.4.3) 1 - fission yeast (Schizosaccharomyces pombe)
N:Alternate names: AtP-AAP transphosphorylase
C:Species: Schizosaccharomyces pombe
C:date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 10-Dec-1999
C:Accession: A46718; T38862; S31338
R:Konrad, M.
J. Biol. Chem. 268, 11326-11334, 1993
A:title: Molecular analysis of the essential gene for adenylate kinase from the fissi
A:Reference number: A46718; MUID:93266590; PMID:8496185
A:Accession: A46718
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-220 <KO2>
A:Cross-references: EMBL:X70363; NID:95535; PIDN:CAA49826.1; PID:95536
A>Note: Sequence extracted from NCBI backbone (NCBITN:132838, NCBIIP:132839)
```


RESULT 9

JCS893

adenylate kinase (EC 2.7.4.3) 2B - human

N:Alternate names: ATP-AMP transphosphorylase

C:Species: Homo sapiens (man)

C:Date: 18-Mar-1998 #sequence_revision 18-Mar-1998 #text_change 18-Jun-1999

C:Accession: JCS893

R:Lee, Y.; Kim, J.W.; Lee, S.M.; Kim, H.J.; Lee, K.S.; Park, C.; Choe, I.S.

J. Biochem. 123, 47-54, 1998

A:Title: Cloning and expression of human adenylate kinase 2 isozymes: Differential expression

A:Reference number: JCS893; MUID:98102934; PMID:9504408

A:Accession: JCS893

A:Molecule type: mRNA

A:Residues: 1-232 <LEE>

A:Cross-references: GB:U54645; NID:q1710886; PIDN:AA13881.1; PID:q1477653

A:Experimental source: tissue fetal liver

C:Comment: This key enzyme is involved in energy metabolism.

C:Genetics:

A:Gene: adk2b

C:Function:

A:Note: magnesium required

C:Superfamily: adenylate kinase

C:Keywords: alternative splicing; ATP; P-loop; phosphotransferase

F:22-29/Region: nucleotide-binding motif A (P-loop) #status atypical

F:95-100/Region: nucleotide-binding motif B #status atypical

F:42-92/Disulfide bonds: #status predicted

F:43,99,145/Active site: His, Asp, His #status predicted

Query Match 37.1%; Score 431; DB 2; Length 232;

Best Local Similarity 43.5%; Pred. No. 4.2e-29;

Matches 87; Conservative 45; Mismatches 62; Indels 6; Gaps 2;

QY 8 LRIVMAGPSGKCTVSSRTTHHELMKHSGLLRNMLRGTEIGVLAFAFDGKLIIP 67

DB 16 IRAVLGPAGKGTQAPRLAENPCVCHLATGDLRAMVAGSLGKRLKATMDAGKLV 75

QY 68 DDVWTRLALHELNK-LTQYSMLDGFPRTPLOAEALD-----RAYQIDTYINLWPREVI 121

DB 76 DEMVVELLEKNLEPPLCKNGFLDGFPRTRYQAEMLDLMKREKLDYSIESIPDLSL 135

QY 122 KQRLTARMIHPASGRVNIENFPKRTVGIDDLGEPFLQREDDKPETVIRKLKAYEDQTK 181

DB 136 IRRITGRILHPKSGRSYHEENPKPEMKDDITGEPLIRSDDEKALKIRLQAYHYQT 195

QY 182 XVLXYOKKGVLETFSGTER 201

DB 196 PLIEYRRKRGHSAIDASQ 215

RESULT 10

G02248

adenylate kinase (EC 2.7.4.3) 2 - human

N:Alternate names: ATP-AMP transphosphorylase

C:Species: Homo sapiens (man)

C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 18-Jun-1999

C:Accession: G02248

R:Choe, I.

submitted to the EMBL Data Library, November 1995

A:Reference number: H00907

A:Accession: G02248

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: mRNA

A:Residues: 1-239 <CHO>

A:Cross-references: EMBL:U3945; NID:q1209686; PIDN:AA13881.1; PID:q1209687

A:Experimental source: tissue fetal liver

C:Genetics:

A:Gene: adk2

C:Function:

A:Note: magnesium required

C:Superfamily: adenylate kinase

C:Keywords: alternative splicing; ATP; P-loop; phosphotransferase

F:22-29/Region: nucleotide-binding motif A (P-loop) #status atypical

F:95-100/Region: nucleotide-binding motif B #status atypical

F:42-92/Disulfide bonds: #status predicted

F:43,99,145/Active site: His, Asp, His #status predicted

Query Match 37.1%; Score 431; DB 2; Length 239;

Best Local Similarity 43.5%; Pred. No. 4.3e-29;

Matches 87; Conservative 45; Mismatches 62; Indels 6; Gaps 2;

QY 8 LRIVMAGPSGKCTVSSRTTHHELMKHSGLLRNMLRGTEIGVLAFAFDGKLIIP 67

DB 16 IRAVLGPAGKGTQAPRLAENPCVCHLATGDLRAMVAGSLGKRLKATMDAGKLV 75

QY 68 DDVWTRLALHELNK-LTQYSMLDGFPRTPLOAEALD-----RAYQIDTYINLWPREVI 121

DB 76 DEMVVELLEKNLEPPLCKNGFLDGFPRTRYQAEMLDLMKREKLDYSIESIPDLSL 135

QY 122 KQRLTARMIHPASGRVNIENFPKRTVGIDDLGEPFLQREDDKPETVIRKLKAYEDQTK 181

DB 136 IRRITGRILHPKSGRSYHEENPKPEMKDDITGEPLIRSDDEKALKIRLQAYHYQT 195

QY 182 XVLXYOKKGVLETFSGTER 201

DB 196 PLIEYRRKRGHSAIDASQ 215

RESULT 11

S61841

adenylate kinase (EC 2.7.4.3) [similarity] - Neisseria meningitidis (strain 22491 ser

N:Alternate names: ATP-AMP transphosphorylase

C:Species: Neisseria meningitidis

A:Variety: strain P63; ATCC 43831

C:Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 02-Feb-2001

C:Accession: S61841; S61842; F81951

R:Valquez, J.A.; Berron, S.; O'Rourke, M.; Carpenter, G.; Fell, E.; Smith, N.H.; Spr

Mol. Microbiol. 15, 1001-1007, 1995

A:Title: Interspecies recombination in nature: a meningococcus that has acquired a g

A:Reference number: S61840; MUID:95349386; PMID:7623657

A:Accession: S61841

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-215 <VAO>

A:Cross-references: EMBL:U36470; NID:9845613; PIDN:AA99173.1; PID:9845614

A:Experimental source: ATCC 43831

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1995

R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mc

Nature 404, 502-506, 2000

A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491

A:Reference number: A81775; MUID:2022556; PMID:10761919

A:Accession: F81951

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-215 <PAR>

A:Cross-references: GB:AL162754; GB:AL157959; NID:97379424; PIDN:CA84301.1; PID:9737

A:Experimental source: serogroup A, strain 22491

C:Genetics:

A:Gene: adk

C:Function:

A:Note: magnesium required

C:Superfamily: adenylate kinase

C:Keywords: ATP; P-loop; phosphotransferase

F:7-14/Region: nucleotide-binding motif A (P-loop) #status atypical

F:80-85/Region: nucleotide-binding motif B #status atypical

F:30,84,126/Active site: Ser, Asp, His #status predicted

Query Match	37.0%;	Score 430;	DB 2;	Length 215;
Best Local Similarity	-45.7%;	Pred. NO. 4.6e-29;		
Matches	86;	Conservative	40;	Mismatches 52;
			Indels	10;
			Gaps	3;

```

QY 8 LRAIVMGPBGKGVSSRITTHPELKLHSGDLLRDMMLGTEGLVAKAFIDOGKIP 67
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 1 MKALLLCPAGCGKGTQAOFTTAFCIPQISTGDMRLRAIKAGTGLGFAKKIIDGGGLVR 60
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 68 DDVM----TFLALHEKLNLTQYSMLLDGFPRTLPQAEAL-DRAYQIDTVNLNVPEVI 121
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 61 DDIITGMVKERIAQDDCKN----GFLFDGFPRTLAQAEAMAEAGVDDDAVVEIDVDSVI 116
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 122 KQRLTARKIHNASGRVNIENPPKTVGIDDLTGEBPLIQEDDKPEVYIKKLAYEDQTK 181
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 117 VDRMSGGRVHVLASGRTHVTVNPNPKVEGKDDVTEGDLIQRDDCKEETGKKRLAYNEOTE 176
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 182 XLVLYYOK 189
   :::::|||||
Db 177 VLVDFTSK 184

```

RESULT 12
E81154

adenylylate kinase NMB0823 [imported] - *Neisseria meningitidis* (strain MC58 serogroup B)
C:Species: *Neisseria meningitidis*
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: F81154
R:Rettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Hatt, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Olt, H.; Vamathavan, J.; Gill, J.; Scarlato, V.; Masingham, V.; Plaza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandt, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V
A:Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
A:Reference number: AB1000; MUID:2015755; PMID:10710307
A:Accession: F81154
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-215 <TET>
A:Cross-references: GB:AE002435; GB:AE002098; NID:g7226049; PIDN:AAF41236.1; PID:g722605
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB0823
A:Superfamily: adenylylate kinase

Query Match	37.0%;	Score 430;	DB 2;	Length 215;
Best Local Similarity	45.7%;	Pred. No. 4.6e-29;		
Matches	86;	Conservative	40;	Mismatches 52; Indels 10; Gaps 3;

Db	1	MAKULLGAPGKGTQAFITAFNGIPQISTGDMLRAAIKAGTPIGLAEAKIIDEGGLVR	60
Qy	68	DDVA-----TRLALHEIKNLQYMSLDDGPPRTLPQAEAL-DRAYQIDYVINTLVNPREVI	121
Db	61	DDILITGKVEKFIADDCKN-----GFLFDGPPRTLAQAEANWAGVDDAVEVIDPDSVI	116
Qy	122	KQRLTARMIHPASGRVYNIENPPKPTVGIDLTGEPLIOREDKDPETVIYKRLKAYEDOTK	181
Db	117	VDRMSGRVHLASRGTLYHVYINPPKVEGKNDVIGEDLIQNDDDKEELIYKRLRAYTHQOTE	176
Qy	182	XVLAAXYQK 189	
Db	177	VLVDEYSK 184	

RESULT 13

adenylylate kinase (EC 2.7.4.3) - *Bordetella pertussis*
N/Alternate names: ATP-AMP transphosphorylase
C/Species: *Bordetella pertussis*
C/Date: 07-Sep-1994 #sequence_revision 10-Nov-1995 #text_change 18-Jun-1999
C/Accession: S43016

R.Gilles, A.M., Sismetro, O.; Munier, H., Fadian, H.; Mantsch, H.H.; Surewicz, W.K.; Eur. J. Biochem. 218, 921-927, 1993
Article: Structural and physico-chemical characteristics of Bordetella pertussis aden
A:Reference number: S43016; MUID:94109391; PMID:8201944

Query Match	36.98;	Score 428;	DB 2;	Length 218;
Best Local Similarity	42.18;	Pred. NO. 6.9e-29;		
Matches	85;	Conservative	45;	Mismatches 64;
			Indels	8;
			Gaps	3;

Oy	8	LRAVMMAPGSGKGVSSRITTHHELKLISGLDRLNMLRGTFIGVLAALFQGLIP	67
	:	::::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::	
Dd	1	MRLIILGPFGAGKGTQAFLYQHGYGIPOISTGDMLRAAVKAATPGLGLEAKVMADAGLVS	60
Oy	68	DDVMTRLALHLELKNTQ---YSWLLDGFPRTLQAEALDRA-YQIDTVNLNVPEVIK	122
	:	: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::	
Dd	61	DDLIIIGLV--RDRLTQPDCAANGYLIFGSPFRPTIQDALMSAGIALDYVEIEVPESDI	117
Oy	123	QRLTRKMTIHPRASGRVYNTEENPPRTVTGIDLTGERPLQREDDKETVYIKRLKAAVEDOTKX	162
	:	::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::	
Dd	118	ERMSERRVRHPASGSRYHNREPNRPKAEAGVDYTGERVLQRDDDEETVRNHRLLNVYQNQTRP	177
Oy	183	VLYXYQQKKGVLETFSGETNKI	204
	:	::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::	
Dd	178	LVDYISSWAQSDAAAAPKYRKI	199

RESULT 14

adenylate kinase (EC 2.7.4.3) - Neisseria gonorrhoeae (strain CH-95)
N:Alternate names: ATP-AMP transphosphorylase
C:Species: Neisseria gonorrhoeae
A:Variety: strain CH-95
C:Date: 27-Apr-1996 #sequence-revision 13-Mar-1997 #text-change 18-Jun-1999
A:Accession: S61843
R:Vaquero, J.A.; Bertron, S.; O'Rourke, M.; Carpenter, G.; Fell, E.; Smith, N.H.; Spratt
Mol. Microbiol. 15, 1001-1007, 1995
A:Title: Intersteps recombination in nature: a meningococcus that has acquired a go
A:Reference number: S61840; MUID:95349386; PMID:7623657
A:Accession: S61843
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-215 (VAZ>
A:Cross-references: EMBL:L36471; NID:9845615; PIDN:AA99174.1; PID:9845616
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1995
C:Superfamily: adenylate kinase
C:Keywords: ATP; P-loop; phosphotransferase
F:7-14/Region: nucleotide-binding motif A (P-loop) #status atypical
F:80-85/Region: nucleotide-binding motif B #status atypical
F:30,84,126/Active site: Ser, Asp, His #status predicted

Query Match	36.6%;	Score 425;	DB 2;	Length 215;
Best Local Similarity	45.7%;	Pred. NO. 1.2e-28;		
Matches 86;	Conservative 40;	Mismatches 52;	Indels 10;	Gaps 3;

```
Oy      8 LRIVIMGAPGSGKGVTSRITTHLELKHLSGDLRLDNMLRTEIGVLAKAFIDOCKLIP 677
      :::::|||||:  ||  :::::||||  :::::  ||  :::  ||  ||  ||  |
Db      1 MKALLIGAPGAGKGTQAOFTAAFGIPQSTGDMLERAIAKAGTPLGLEKKIIDEGLVR 600
```

```

QY 68 DDVM-----TRLALHELKLNLTQYSMLLDGFPRTLPOAEAL-DRAYQIDFYINLNVPEFYI 121
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 61 DDIIIGMVKERINQDDCKN-----GFLFDGFPRTLQAENAVENGVLDAVEIDVSDSYI 116
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY 122 KQRLTKRWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDDKPETVIKRLKAYEDQTK 181
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 117 VDRMSGRRVHLASGRTHVYTNPPKTEGKDDVYTGEDLIQRDDDKETVKKRLAVYHQTE 176
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY 182 XVLYXYXQK 189
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 177 VLVDFTYSK 184
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||

```

RESULT 15

```

G83184
adenylate kinase PA3686 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: G83184
R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapid, K.; Lam,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: G83184
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-215 <STO>
A:Cross-references: GB:AE004788; GB:AE004091; NID:g9949846; PIDN:AA07074.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: adk; PA3686
C:Superfamily: adenylate kinase

```

```

Query Match          36.5%; Score 424; DB 2; Length 215;
Best Local Similarity 46.6%; Pred. 1.5e-28;
Matches 88; Conservative 29; Mismatches 70; Indels 2; Gaps 2;

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QY 8. LRAVINGAPGSGKGVSSRTTTHFEKLHSSGDLRLDNMLRGTEIGVLAKAFIDGKLIIP 67
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 1 MRVILGAPGAGCGTQARFITEKFIPOISTGDMLEAAVAGSPICQVKGVMDSGLVS 60
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY 68 DDVMTRLALHELKLNLTQYSMLLDGFPRTLPOAEAL-DRAYQIDFYINLNVPEFYIKQRL 125
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 61 DDIIIGMVKERINQDDCKN-----GFLFDGFPRTLQAENAVENGVLDAVEIDVSDSYI 120
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Y 126 TARKWHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDDKPETVIKRLKAYEDQTKXVLYK 185
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 121 AGRVHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDDKPETVIKRLKAYEDQTKXVLYK 180
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY 186 YVOKKGVLE 194
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 181 FYOKLSAAE 189
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||

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Search completed: March 19, 2003, 16:44:32
Job time : 694 secs

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GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 19, 2003, 13:35:59 ; Search time 314 Seconds

(without alignments)
29.984 Million cell updates/sec

Title: US-10-006-190-1

Perfect score: 1161

Sequence: 1 MGASARLRAVIMGAPGSGK.....VYAFLOTXVPORSQKASVTP 227

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1123	96.7	226	1	KAD3_HUMAN
2	1086	93.5	226	1	KAD3_BOVIN
3	1046	90.1	219	1	KAD3_MOUSE
4	1033	89.0	226	1	KAD3_RAT
5	708.5	61.0	223	1	KAD4_MOUSE
6	708.5	61.0	223	1	KAD4_MOUSE
7	700.5	60.3	223	1	KAD4_MOUSE
8	447.5	38.3	214	1	KAD4_HUMAN
9	445	38.3	222	1	KAD4_HUMAN
10	440.5	37.9	224	1	KAD4_HUMAN
11	439.5	37.9	225	1	KAD4_HUMAN
12	438	37.7	246	1	KAD4_HUMAN
13	437	37.6	217	1	KAD4_HUMAN
14	436	37.6	220	1	KAD4_HUMAN
15	435	37.5	221	1	KAD4_HUMAN
16	435	37.5	221	1	KAD4_HUMAN
17	431	37.1	238	1	KAD4_HUMAN
18	430	37.0	215	1	KAD4_HUMAN
19	428	36.9	218	1	KAD4_HUMAN
20	428	36.9	243	1	KAD4_HUMAN
21	425	36.6	243	1	KAD4_HUMAN
22	424	36.5	215	1	KAD4_HUMAN
23	421	36.3	236	1	KAD4_HUMAN
24	419	36.1	240	1	KAD4_HUMAN
25	417.5	36.0	218	1	KAD4_HUMAN
26	417	35.9	215	1	KAD4_HUMAN
27	417	35.9	215	1	KAD4_HUMAN
28	416	35.8	215	1	KAD4_HUMAN
29	416	35.8	251	1	KAD4_HUMAN
30	415	35.7	238	1	KAD4_HUMAN
31	413	35.6	214	1	KAD4_HUMAN
32	408	35.1	215	1	KAD4_HUMAN
33	407	35.1	215	1	KAD4_HUMAN

34	405	34.9	214	1	KAD4_HUMAN	P05082 escherichia
35	401.5	34.6	214	1	KAD4_HUMAN	09kt7 vibrio chol
36	401	34.5	216	1	KAD4_HUMAN	092409 pseudomonas
37	401	34.5	217	1	KAD4_HUMAN	P16304 bacillus su
38	400	34.5	214	1	KAD4_HUMAN	069172 yersinia pe
39	397	34.2	231	1	KAD4_HUMAN	09wt6 mus musculu
40	395.5	34.1	217	1	KAD4_HUMAN	029581 archaeglob
41	395	34.0	222	1	KAD4_HUMAN	009629 caenorhabdi
42	393	33.9	206	1	KAD4_HUMAN	066480 aquilex aeo
43	389	33.5	200	1	KAD4_HUMAN	P43412 streptomyce
44	383.5	33.0	214	1	KAD4_HUMAN	P43412 yersinia en
45	379	32.6	174	1	KAD4_HUMAN	059594 neisseria c

ALIGNMENTS

RESULT 1	ID	Sequence	Score	Length	DB	Match	Query Match	Length	ID	Description
KAD3_HUMAN	1	1123	96.7	226	1	KAD3_HUMAN	96.7	226	1	KAD3_HUMAN
KAD3_HUMAN	2	1086	93.5	226	1	KAD3_BOVIN	93.5	226	1	KAD3_BOVIN
KAD3_HUMAN	3	1046	90.1	219	1	KAD3_MOUSE	90.1	219	1	KAD3_MOUSE
KAD3_HUMAN	4	1033	89.0	226	1	KAD3_RAT	89.0	226	1	KAD3_RAT
KAD3_HUMAN	5	708.5	61.0	223	1	KAD4_MOUSE	61.0	223	1	KAD4_MOUSE
KAD3_HUMAN	6	708.5	61.0	223	1	KAD4_MOUSE	61.0	223	1	KAD4_MOUSE
KAD3_HUMAN	7	700.5	60.3	223	1	KAD4_MOUSE	60.3	223	1	KAD4_MOUSE
KAD3_HUMAN	8	447.5	38.3	214	1	KAD4_HUMAN	38.3	214	1	KAD4_HUMAN
KAD3_HUMAN	9	445	38.3	222	1	KAD4_HUMAN	38.3	222	1	KAD4_HUMAN
KAD3_HUMAN	10	440.5	37.9	224	1	KAD4_HUMAN	37.9	224	1	KAD4_HUMAN
KAD3_HUMAN	11	439.5	37.9	225	1	KAD4_HUMAN	37.9	225	1	KAD4_HUMAN
KAD3_HUMAN	12	438	37.7	246	1	KAD4_HUMAN	37.7	246	1	KAD4_HUMAN
KAD3_HUMAN	13	437	37.6	217	1	KAD4_HUMAN	37.6	217	1	KAD4_HUMAN
KAD3_HUMAN	14	436	37.6	220	1	KAD4_HUMAN	37.6	220	1	KAD4_HUMAN
KAD3_HUMAN	15	435	37.5	221	1	KAD4_HUMAN	37.5	221	1	KAD4_HUMAN
KAD3_HUMAN	16	435	37.5	221	1	KAD4_HUMAN	37.5	221	1	KAD4_HUMAN
KAD3_HUMAN	17	431	37.1	238	1	KAD4_HUMAN	37.1	238	1	KAD4_HUMAN
KAD3_HUMAN	18	430	37.0	215	1	KAD4_HUMAN	37.0	215	1	KAD4_HUMAN
KAD3_HUMAN	19	428	36.9	218	1	KAD4_HUMAN	36.9	218	1	KAD4_HUMAN
KAD3_HUMAN	20	428	36.9	243	1	KAD4_HUMAN	36.9	243	1	KAD4_HUMAN
KAD3_HUMAN	21	425	36.6	243	1	KAD4_HUMAN	36.6	243	1	KAD4_HUMAN
KAD3_HUMAN	22	424	36.5	215	1	KAD4_HUMAN	36.5	215	1	KAD4_HUMAN
KAD3_HUMAN	23	421	36.3	236	1	KAD4_HUMAN	36.3	236	1	KAD4_HUMAN
KAD3_HUMAN	24	419	36.1	240	1	KAD4_HUMAN	36.1	240	1	KAD4_HUMAN
KAD3_HUMAN	25	417.5	36.0	218	1	KAD4_HUMAN	36.0	218	1	KAD4_HUMAN
KAD3_HUMAN	26	417	35.9	215	1	KAD4_HUMAN	35.9	215	1	KAD4_HUMAN
KAD3_HUMAN	27	417	35.9	215	1	KAD4_HUMAN	35.9	215	1	KAD4_HUMAN
KAD3_HUMAN	28	416	35.8	215	1	KAD4_HUMAN	35.8	215	1	KAD4_HUMAN
KAD3_HUMAN	29	416	35.8	251	1	KAD4_HUMAN	35.8	251	1	KAD4_HUMAN
KAD3_HUMAN	30	415	35.7	238	1	KAD4_HUMAN	35.7	238	1	KAD4_HUMAN
KAD3_HUMAN	31	413	35.6	214	1	KAD4_HUMAN	35.6	214	1	KAD4_HUMAN
KAD3_HUMAN	32	408	35.1	215	1	KAD4_HUMAN	35.1	215	1	KAD4_HUMAN
KAD3_HUMAN	33	407	35.1	215	1	KAD4_HUMAN	35.1	215	1	KAD4_HUMAN

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OY 122 KORLTARWHPASGRVYNIEFNPCKTVGIDDLTGEPLIQEDDKPEYVIRLKAAYEDQK 181
DB 121 KORLTARWHPASGRVYNIEFNPCKTVGIDDLTGEPLIQEDDKPEYVIRLKAAYEDQK 180
OY 182 XVLXYOKKGVLTFSGTETNKIMPYVAFLOTKVPORSOKASVTP 227
DB 181 PULEYTRKKGVLETFSGTETNKIMPYVAFLOTKVPORSOKASVTP 226

RESULT 2
KAD3_BOVIN STANDARD: PRT: 226 AA.
AC P08760;
DT 01-NOV-1988 (rel. 09, Created)
DT 01-APR-1990 (rel. 14, Last sequence update)
DT 01-NOV-1997 (rel. 35, Last annotation update)
DE GTP:AMP phosphotransferase mitochondrial (EC 2.7.4.10) (AK3).
GN AK3.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90037053; PubMed=2478555;
RA Yamada M., Shahjahan M., Tanabe T., Kishi F., Nakazawa A.;
RT "Cloning and characterization of cDNA for mitochondrial GTP:AMP
RT phosphotransferase of bovine liver."
RL J. Biol. Chem. 264:19192-19199(1989).
RN [2]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=86248102; PubMed=3013690;
RA Tomasselli A.G., Frank R., Schiltz E.;
RT "The complete primary structure of GTP:AMP phosphotransferase from
RT beef heart mitochondria."
RL FEBS Lett. 202:303-308(1986).
RN [3]
RP SEQUENCE OF 1-49 FROM N.A.
RX MEDLINE=92084124; PubMed=1748300;
RA Shahjahan M., Yamada M., Tanaka H., Nakazawa A.;
RT "Cloning and characterization of the gene encoding bovine
RT mitochondrial adenylate kinase isozyme 3."
RL Gene 107:313-317(1991).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=91084487; PubMed=2175649;
RA Diederichs K., Schulz G.E.;
RT "Three-dimensional structure of the complex between the mitochondrial
RT matrix adenylate kinase and its substrate AMP."
RL Biochemistry 29:8138-8144(1990).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS).
RX MEDLINE=91132661; PubMed=1994037;
RA Diederichs K., Schulz G.E.;
RT "The refined structure of the complex between adenylate kinase from
RT beef heart mitochondrial matrix and its substrate AMP at 1.85-A
RT resolution."
RL J. Mol. Biol. 217:541-549(1991).
CC -1- CATALYTIC ACTIVITY: GTP + AMP -> GDP + ADP.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
CC -----
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DR EMBL: D10376; BAA01210.1; -.
DR EMBL: D10373; BAA01210.1; JOINED.
DR EMBL: D10374; BAA01210.1; JOINED.
DR EMBL: D10375; BAA01210.1; JOINED.
DR EMBL: M25757; AAA30705.1; -.
DR PIR: A24201; A24201.
DR PIR: A34442; A34442.
DR PIR: JH0512; JH0512.
DR PDB: 2AK3; 12-MAY-95.
DR InterPro: IPR000850; Adenylate_kin.
DR Pfam: PF00406; Adenylate_kin.
DR PRINTS: PR00094; ADENYLKINASE.
DR ProDom: PD000657; Adenylate_kin. 1.
DR PROSITE: PS00113; ADENYLATE_KINASE. 1.
KW Transferase; Kinase; GTP-binding; Mitochondrion; 3D-structure.
FT INIT MET 0
FT NP_BIND 13 21 GTP (BY SIMILARTY).
FT CONFLICT 10 10 MISSING (IN REF. 2).
FT STRAND 8 12
FT TURN 15 16
FT HELIX 19 29
FT STRAND 33 36
FT HELIX 37 45
FT TURN 46 48
FT HELIX 50 60
FT TURN 61 62
FT HELIX 67 79
FT TURN 80 81
FT STRAND 86 89
FT HELIX 95 102
FT TURN 103 104
FT STRAND 109 114
FT HELIX 117 124
FT TURN 125 125
FT STRAND 127 130
FT TURN 131 134
FT STRAND 135 138
FT TURN 139 141
FT STRAND 142 142
FT TURN 142 148
FT STRAND 149 149
FT TURN 151 153
FT STRAND 156 156
FT STRAND 158 158
FT TURN 161 162
FT HELIX 165 189
FT TURN 190 190
FT STRAND 192 196
FT HELIX 200 212
FT TURN 213 214
SQ SEQUENCE 226 AA; 25540 MW; 2B74C2PBAAAC7CBA9 CRC64;

Query Match 93.5%; Score 1086; DR 1; Length 226;
Best Local Similarity 91.6%; Pred. No. 1,5e-86;
Matches 207; Conservative 10; Mismatches 9; Indels 0; Gaps 0;
OY 2 GASARLLRAVINGAPSGRGVSSRTTTFELKHLSSGDLRDNMGRTEIGVLAKAFID 61
DB 1 GASARLLRAVINGAPSGRGVSSRTTTFELKHLSSGDLRDNMGRTEIGVLAKTFID 60
OY 62 GSKLIPDDVWTRVLALHELKNTLYQSWLDGFPRTLPOAEBALDRAYQIDTVIMLWPFVEYI 121
DB 61 GSKLIPDDVWTRVLALHELKNTLYQSWLDGFPRTLPOAEBALDRAYQIDTVIMLWPFVEYI 120
OY 122 KORLTARWHPASGRVYNIEFNPCKTVGIDDLTGEPLIQEDDKPEYVIRLKAAYEDQK 181
DB 121 KORLTARWHPASGRVYNIEFNPCKTVGIDDLTGEPLIQEDDKPEYVIRLKAAYEDQK 180
OY 182 XVLXYOKKGVLTFSGTETNKIMPYVAFLOTKVPORSOKASVTP 227
DB 181 PULEYTRKKGVLETFSGTETNKIMPYVAFLOTKVPORSOKASVTP 226

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RESULT 3
KAD3_MOUSE
ID KAD3_MOUSE STANDARD: PRT: 219 AA.
AC Q9WTP7: 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE GTP:AMP phosphotransferase mitochondrial (EC 2.7.4.10) (AK3)
DE (Fragment)
GN AK3 OR AK-3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Noma T.;
RL Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: GTP + AMP -> GDP + ADP.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: AB020203; BAA77360.1; -.
CC DR HSSP: P08760; 2AK3.
CC DR MGI: 87979; AK3.
CC DR InterPro: IPR000850; Adenylate_kin.
CC DR Pfam: PF00406; adenylatekinase.1.
CC DR PRINTS: PR00094; ADENYLTKINASE.
CC DR ProDom: PD000657; Adenylate_kin.1.
CC DR PROSITE: PS00113; ADENYLATE_KINASE.1.
CC KW Transferase; kinase; GTP-binding; Mitochondrion.
CC FT NON_TER 1 1
CC FT NP_BIND 6 14 GTP (BY SIMILARITY).
CC SQ SEQUENCE 219 AA; 24640 MW; 7DDB8DFA2C0EE7C5 CRC64;

Query Match 90.1%; Score 1046; DB 1; Length 219;
Best Local Similarity 92.2%; Pred. No. 4e-83;
Matches 202; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 9 RAVINGAPSGSGKGVSSRTTHFELKHLSSGDLRLRNMLRGTEIGVAKAFIDGKLIIP 68
DB 1 RAVINGAPSGSGKGVSSRTTHFELKHLSSGDLRLRNMLRGTEIGVAKAFIDGKLIIP 60
QY 69 DWVTRLALHELKNTQYSWLDGFPRTLPOAEALDRAYQIDIVINLVPEVVKORLTAR 128
DB 61 DWVTRLALHELKNTQYSWLDGFPRTLPOAEALDRAYQIDIVINLVPEVVKORLTAR 120
QY 129 WTHPASGRVYNIEFNPVKTVGIDDLTGEPILQREDKPETVIKRLAYEDQTXVLYYQ 188
DB 121 WTHPASGRVYNIEFNPVKTVGIDDLTGEPILQREDKPETVIKRLAYEDQTXVLYYQ 180
QY 189 KKGVLTFSGTETNKIMPVYVAFLOTKVPORSOKASVTP 227
DB 181 KKGVLTFSGTETNKIMPVYVAFLOTKVPORSOKASVTP 219

RESULT 4
KAD3_RAT
ID KAD3_RAT STANDARD: PRT: 226 AA.
AC P29411: 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE GTP:AMP phosphotransferase mitochondrial (EC 2.7.4.10) (AK3).

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GN AK3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Tanabe T., Yamada M., Noma T., Kajii T., Nakazawa A.;
RT "Tissue-specific and developmentally regulated expression of the
RT gene encoding adenylate kinase isozymes."
RL J. Biochem. 113:200-207(1993).
CC -1- CATALYTIC ACTIVITY: GTP + AMP -> GDP + ADP.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: D13062; BAA02379.1; -.
CC DR PIR: J01945; J01945.
CC DR HSSP: P08760; 2AK3.
CC DR InterPro: IPR000850; Adenylate_kin.
CC DR Pfam: PF00406; adenylatekinase.1.
CC DR PRINTS: PR00094; ADENYLTKINASE.
CC DR ProDom: PD000657; Adenylate_kin.1.
CC DR PROSITE: PS00113; ADENYLATE_KINASE.1.
CC KW Transferase; kinase; GTP-binding; Mitochondrion.
CC FT INIT_MET 0 0 BY SIMILARITY.
CC FT NP_BIND 13 21 GTP (BY SIMILARITY).
CC SQ SEQUENCE 226 AA; 25307 MW; D57FE37404AA6625 CRC64;

Query Match 89.0%; Score 1033; DB 1; Length 226;
Best Local Similarity 90.3%; Pred. No. 5.4e-82;
Matches 204; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 2 GASARLLRAVIMAPSGSGKGVSSRTTHFELKHLSSGDLRLRNMLRGTEIGVAKAFID 61
DB 1 GASARLLRAVIMAPSGSGKGVSSRTTHFELKHLSSGDLRLRNMLRGTEIGVAKAFID 60
QY 62 QGKLIPDDVTRLALHELKNTQYSWLDGFPRTLPOAEALDRAYQIDIVINLVPEVY 121
DB 61 QGKLIPDDVTRLALHELKNTQYSWLDGFPRTLPOAEALDRAYQIDIVINLVPEVY 120
QY 122 KORLTARWTHPASGRVYNIEFNPVKTVGIDDLTGEPILQREDKPETVIKRLAYEDQTX 181
DB 121 KORLTARWTHPASGRVYNIEFNPVKTVGIDDLTGEPILQREDKPETVIKRLAYEDQTX 180
QY 182 XVLXYQKKGVLTFSGTETNKIMPVYVAFLOTKVPORSOKASVTP 227
DB 181 XVLXYQKKGVLTFSGTETNKIMPVYVAFLOTKVPORSOKASVTP 226

RESULT 5
KAD4_MOUSE
ID KAD4_MOUSE STANDARD: PRT: 223 AA.
AC Q9WUR9: 09-1X7: 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Adenylate kinase isoenzyme 4, mitochondrial (EC 2.7.4.3) (ATP-AMP
DE transphosphorylase).
GN AK4 OR AK-4 OR AK3B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

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RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE-Brain:
RX      MEDLINE=99033072; PubMed=9813119;
RY      Yoneda T., Sato M., Maeda M., Takagi H.;
RT      Identification of a novel adenylylate kinase system in the brain:
RL      cloning of the fourth adenylylate kinase";
RN      Brain Res. Mol. Brain Res. 62:187-195(1998).
RP      [2]
RP      SEQUENCE FROM N.A.
RA      Noma T.;
RL      Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RC      -1- CATALYTIC ACTIVITY: GRP + AMP = GDP + ADP.
CC      -1- SUBCELLULAR LOCATION: Mitochondrial matrix (potential).
CC      -1- TISSUE SPECIFICITY: EXPRESSED IN THE PYRAMIDAL CELLS IN THE
CC      HIPPOCAMPUS.
CC      -1- DEVELOPMENTAL STAGE: EXPRESSED IN THE CENTRAL NERVOUS SYSTEM IN A
CC      REGION-SPECIFIC MANNER FROM THE MIDDLE STAGE OF EMBRYOGENESIS TO
CC      THE ADULTHOOD IN THE RODENT.
CC      -1- SIMILARITY: BELONGS TO THE ADENYLYATE KINASE FAMILY.
CC      -----
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CC      -----
DR      EMBL; D85036; BAA77760.1; -.
DR      EMBL; AB020239; BAA77363.1; -.
DR      HSSP; P08760; 2AK3.
DR      MGD; MGI:87980; AK4.
DR      InterPro: IPR000850; Adenylylate_kin.
DR      Pfam; PF00406; adenylylatekinase; 1.
DR      PRINTS; PR00094; ADENYLYL_KINASE.
DR      ProDom; PD000657; Adenylylate_kin; 1.
DR      PROSITE; PS00113; ADENYLYLATE_KINASE; 1.
KW      Transferase; Kinase; GTP-binding; Mitochondrion.
FT      NP_BIND 12 20 GTP (BY SIMILARITY).
FT      CONFLICT 68 68 V -> A (IN REF. 2).
FT      CONFLICT 187 187 S -> N (IN REF. 2).
FT      CONFLICT 190 190 V -> M (IN REF. 2).
SQ      SEQUENCE 223 AA; 25061 MW; 50552294971515EC CRC64;

Query Match 61.0%; Score 708.5; DB 1; Length 223;
Best Local Similarity 58.8%; Pred. No. 4.7e-54;
Matches 130; Conservative 41; Mismatches 49; Indels 1; Gaps 1;

OY      4 SARLLRAVIMGPPGSGKGVSSRTITHEPLKILSSGDDLRLDMLGTEGLAKAFIDGG 63
      :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB      2 ASKLIRAVIILGPPGSGKGVSCRIKQNGDLHSSGCHLRNMLKTKTEVGDVAKQYLEGG 61
OY      64 KLIPDVMTRLALHLEKLNLTQYSWLLDGFPRRTLPOAELADRAYQIDTYINLWPREVIKQ 123
      :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB      62 LLVPRVHTLRILMSLELERSAQHMLLDGFPRTLVQAELADGICVDVLYSLNIPRETLKD 121
OY      124 RLTAWHIPASGRVYNIENFPKTYGIDDLGERPLIQEDDKPREVYIKRLAYEQGTXXY 183
      ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB      122 RLSRWMIHPSSGRVYNLDPNPQVQIDITGEPVQOEDDKPEVAARLRLRYKDAARPV 181
OY      184 LAYYOKKGVLETFSGTETNKIKIPYVYAEIQTQV-PQRSOKA 223
      :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB      182 TELYKSRGVLFHOFSGTETNRIIMPVYVYTFLESNKITPTIQSNEA 222

RESULT 6
KADA__RAT
ID      KADA__RAT      STANDARD:      PRT:      223 AA.
AC      Q9WU50:
DT      30-MAY-2000 (Rel. 39, Created)
DT      30-MAY-2000 (Rel. 39, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)

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DE Adenylate kinase isoenzyme 4, mitochondrial (EC 2.7.4.3) (ATP-AMP
DE transphosphorylase).
GN AK4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Forebrain;
RX MEDLINE=99033072; PubMed=9813319;
Yoneeda T., Sato M., Maeda M., Takagi H.;
RT "Identification of a novel adenylate kinase system in the brain:
RT cloning of the fourth adenylate kinase.";
RL Brain Res. Mol. Brain Res. 62:187-195(1998).
CC -1- CATALYTIC ACTIVITY: GTP + AMP = GDP + ADP.
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix (potential).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE PYRAMIDAL CELLS IN THE
CC HIPPOCAMPUS.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN THE CENTRAL NERVOUS SYSTEM IN A
CC REGION-SPECIFIC MANNER FROM THE MIDDLE STAGE OF EMBRYOGENESIS TO
CC THE ADULTHOOD IN THE RODENT.
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
CC -----
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CC -----
CC EMBL: D87809; BAA77761.1; -.
DR HSSP: P08760; ZAK3.
DR InterPro: IPR000850; Adenylate_kin.
DR Pfam: PF00406; adenylatekinase.1.
DR PRINTS: PR00094; ADENYLTKINASE.
DR ProDom: PD000657; Adenylate_kin.1.
DR PROSITE: PS00113; ADENYLATE_KINASE; 1.
KW Transferase; Kinase; GTP-binding; Mitochondrion.
FT NP_BIND 12 20 GTP (BY SIMILARITY).
SQ
SEQUENCE 223 AA; 25203 MW; B5A9BB45CFA3C19B CMC64;

Query Match 61.0%; Score 708.5; DB 1; Length 223;
Best Local Similarity 57.9%; Pred. No. 4.7e-54;
Matches 128; Conservative 44; Mismatches 48; Indels 1; Gaps 1;

OY 4 SARLRRAVIMVPGSGGKGVSSRTITHEELKLSSGDLRDNMLGTEIGVLAKAFLIDOG 63
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
DB 2 ASKLRAVILTSPGSGKGVTCERINQNGLOHLSHGHLRLRLKNTVEVGVAQYLEKG 61
OY 64 KLIPDDVMTRLALHELKLNLTQYSMLDGFPPRLTPOAEALDRAYQIDYINLVNPPREVKQ 123
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
DB 62 LLYPVHYITRLMSELERSAQHMLLDGFPPRLTVQAEALDRICDDVDVLSINIPETLKK 121
OY 124 RLTAAMIPHAGSRVYNIENPKPTGVGIDDLGCEPLIOGEDDKPETVIKRLAAYEDQTKXV 183
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
DB 122 KLSRKHHPSSGRVYNLDNPPQVLGVGDITGEPLVQGEDDKPELALRLRYDAKPV 181
OY 184 LXXYQKGVLETFSGETFNKIMPVYAEFLQTKV-PORSOKA 223
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
DB 182 IELYKSRGVLFHQSGETETNRIMPVYTVLFSSNKTPTIQSKEA 222

RESULT 7
KADA_HUMAN STANDARD; PRT; 223 AA.
AC P27144;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Adenylate kinase isoenzyme 4, mitochondrial (EC 2.7.4.3) (ATP-AMP
DE transphosphorylase).

```

GN AK4 OR AK3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92347846; PubMed=1639383;
RA Xu G., O'Connell P., Stevens J., White R.;
RT "Characterization of human adenylylate kinase 3 (AK3) cDNA and mapping
RL of the AK3 pseudogene to an intron of the NFI gene.";
RN Genomics 13:537-542(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: GTP + AMP = GDP + ADP.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
CC -----
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CC -----
DR EMBL; X60673; CAA43088.1; -;
DR EMBL; BC016180; AAH16180.1; -;
DR PIR; S16381; S16381.
DR PIR; S16380; S16380.
DR PIR; A42820; A42820.
DR HSP; P08760; ZAK3.
DR Genew; HGNC:363; AK3.
DR MIM; 103030; -;
DR InterPro: IPR000850; Adenylylate_kin.
DR Pfam: PF00406; adenylylatekinase; 1.
DR PRINTS; PR00094; ADENYLTKINASE.
DR Prodom; PD000657; Adenylylate_kin; 1.
DR PROSITE; PS00113; ADENYLATE_KINASE; 1.
KW Transferase; Kinase; GTP-binding; Mitochondrion.
FT NP_BIND 12 GTP (BY SIMILARITY).
SQ SEQUENCE 223 AA; 25268 MW; 65341A8EB3BC723 CRC64;
Query Match 60.3%; Score 700.5; DB 1; Length 223;
Best Local Similarity 58.8%; Pred. No. 2.3e-53;
Matches 130; Conservative 38; Mismatches 52; Indels 1; Gaps 1;
OY 4 SARLLRAVINGAPSGSGKTVSSRTTHFEKLHSSGDLRLDNLRGTEIGVLAFAFDIG 63
DB 2 ASKLLRAVITLPPGSGKTVSSRTTHFEKLHSSGDLRLDNLRGTEIGVLAFAFDIG 61
OY 64 KLIDPDVMTRLALHELKNTLYSWLDDGFPRTLPOAERLADRAYOIVTINLVNPEVYKQ 123
DB 62 LLYVDVHTITRLMSELEKRRQHWLDDGFPRTLPOAERLADRAYOIVTINLVNPEVYKQ 121
OY 124 RLTAARWHPASGRVYNIENFPKTVGIDDLTGEPLIQREDKPETVIKRLKAYEDQTKV 183
DB 122 RLSRRWHPASGRVYNIENFPKTVGIDDLTGEPLIQREDKPETVIKRLKAYEDQTKV 181
OY 184 LXYQKKGVLTEFSGTEKNTWYVYAFLOTKV-PORSOKA 223
DB 182 IELYKSRGVLLHQFSGTEKNTWYVYAFLOTKV-PORSOKA 222
RESULT 8
KAD_HAEIN STANDARD; PRT; 214 AA.
AC P24323;
DT 01-MAR-1992 (Rel. 21, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Adenylylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).
GN AK4 OR H10349.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RM 7004 / Serotype B;
RX MEDLINE=92065797; PubMed=1956282;
RA Maskell D.J., Szabo M.J., Butler P.D., Williams A.E., Moxon E.R.;
RT "Molecular analysis of a complex locus from Haemophilus influenzae
RL involved in phase-variable lipopolysaccharide biosynthesis.";
RN Mol. Microbiol. 5:1013-1022(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=RM 7004 / ATCC 51907;
RX MEDLINE=9530630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Knelavage A.R., Bult C.J., Tomb J.F., Dougherty B.A., Merrick J.M.,
RA McEweney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Sauder D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fritchman J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RL Rd.";
RN Science 269:496-512(1995).
CC -1- FUNCTION: THIS SMALL UBICUITOUS ENZYME IS ESSENTIAL FOR
CC MAINTENANCE AND CELL GROWTH. IT MAY BE LINKED TO THE BIOSYNTHESIS
CC OF LIPOPOLYSACCHARIDE SURFACE MOLECULES, WHICH ARE IMPORTANT FOR
CC THE PATHOGENESIS OF H. INFLUENZAE.
CC -1- CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
CC -----
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CC -----
DR EMBL; X57315; CAA40570.1; -;
DR EMBL; U32719; AAC22010.1; -;
DR PIR; S15280; S15280.
DR HSP; P05082; IEAY.
DR TIGR; H10349; -;
DR InterPro: IPR000850; Adenylylate_kin.
DR Pfam: PF00406; adenylylatekinase; 1.
DR PRINTS; PR00094; ADENYLTKINASE.
DR Prodom; PD000657; Adenylylate_kin; 1.
DR PROSITE; PS00113; ADENYLATE_KINASE; 1.
KW Transferase; Kinase; ATP-binding; Complete proteome.
FT NP_BIND 7 78 T -> A (IN REF. 1).
SQ SEQUENCE 214 AA; 23508 MW; B83B630EE9E1AAFC CRC64;
Query Match 38.5%; Score 447.5; DB 1; Length 214;
Best Local Similarity 46.1%; Pred. No. 1.3e-31;
Matches 95; Conservative 37; Mismatches 61; Indels 13; Gaps 4;
OY 8 LRAVIMGAPSGSGKTVSSRTTHFEKLHSSGDLRLDNLRGTEIGVLAFAFDIGKILP 67
DB 1 KRIILGAPGAGKTVQAOAIVNNKRGIPQISTGDMFAIKAGTEIGKQAKALMDGKILP 60
OY 68 DD-----VMTRLALHELKNTLYSWLDDGFPRTLPOAERLADRAYOIVTINLVNPEVY 121

D _b	61	DELVALAKDRILAQADCN-----GELLDSFPRTIQADALDKDSVKIDFVLEEDVPREVI	116
Q _y	122	KQRLTARHHPASGRVNIENPPKTVGIDDLTGEPLIQREDDKPEYIVKRLAYEEDQTK	181
D _b	117	VERMSGRRVHVASGRSRSHIYVNPKEVGEKGDVDTGEDLIRADDKPEYIVDLRLAYVHKOTS	176
Q _y	182	XVLKYYO---KKGLTEFSGSETNKI	204
D _b	177	PLIDYQAEAKAGNTQYFRDLDTGTOK	202

RESULT 9
KAD BAI.SC

ID	KAD_RALSO	STANDARD;	PRT;	222 AA.
AC	08XWEL;			
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Adenylylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).			
GN	ADK OR RSC2533 OR RS05765.			
OS	Ralstonia solanacearum (Pseudomonas solanacearum).			
OC	Bacteria; Proteobacteria; beta subdivision; Ralstonia group;			
OC	Ralstonia.			
OX	NCBI_TaxID=305;			
ON	131			

RP SEQUENCE FROM N.A.
RC STRAIN-GM1100;
RX MEDLINE-21681879; PubMed-11823852;
RA Salanoubat M., Genin S., Artiguenave F., Guzy J., Mangenot S.,
RA Ariat M., Billault A., Brottier P., Camus J.C., Catilico L.,
RA Chandier M., Chloime N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Molisan A., Robert C., Saurin W., Schlex T.,
RA Sluiter C., Thebaud P., Whalen M., Wincker P., Levy M.,
RA Weissensbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen *Ralstonia solanacearum*";
RL Nature 415:497-502(2002).
CC -1- FUNCTION: This small ubiquitous enzyme is essential for
CC maintenance and cell growth.
CC -1- CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.

[illegible]

RESULT 10

ID	KAD_PASMU	STANDARD;	PRT;	214 AA.
AC	p57837;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Adenylylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).			
GN	ADK OR PM0284.			
OS	Pasteurella multocida.			
OC	Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae			
OC	Pasteurella.			
OX	NCBI_Taxid=747;			
RN	[1]			
RP	SEQUENCE FROM N.A.			

CC STRAIN:PM70;
CC MEDLINE:21145866; PubMed:11248100;
CC May B.J., Zhang Q., Li L.L., Pausitan M.L., Whitam T.S., Kapur V. ;
CC "Complete genomic sequence of *Pasteurella multocida* Pm70." ;
CC Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC -1- FUNCTION: THIS SMALL UBICUITOUS ENZYME IS ESSENTIAL FOR
CC MAINTENANCE AND CELL GROWTH.
CC -1- CATALYTIC ACTIVITY: ATP + AMP -> ADP + ADP.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ADENYLYATE KINASE FAMILY.
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DB 181 YXQAEKAGNTKVFRLDGTKKV 202

RESULT 11
KAD2_YEAST STANDARD: PRT: 225 AA.

AC P26364;
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUL-1992 (Rel. 36, Last annotation update)
DE Adenylate kinase 2 (EC 2.7.4.3) (ATP-AMP transphosphorylase).
GN ADK2 OR PAK3 OR YER170W.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycos.
OX NCBI_TaxId=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-92267376; PubMed-1587477;
RA Cooper A.J., Friedberg E.C.;
RT "A putative second adenylate kinase-encoding gene from the yeast
RT Saccharomyces cerevisiae."
RL Gene 114:145-148(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-92318888; PubMed-1620094;
RA Schlicker R., Magdolen V., Bandlow W.;
RT "A new member of the adenylate kinase family in yeast: PAK3 is highly
RT homologous to mammalian AK3 and is targeted to mitochondria."
RL Mol. Gen. Genet. 233:363-371(1992).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN-S286C / AB972;
RA Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R.,
RA Aviles E., Beruo A., Brennan T., Carpenter J., Chen E., Cherry J.M.,
RA Chung E., Duncan M., Guman E., Hartzell G., Hunnicke-Smith S.,
RA Hymen R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Mosedale D., Nakahara K., Namath A., Norgren R., Oetner P., Oh C.,
RA Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V.,
RA Taylor P., Wei Y., Yellon M., Botstein D., Davis R.W.;
RL Submitted (DEC-1994) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR
CC MAINTENANCE AND CELL GROWTH.
CC -1- CATALYTIC ACTIVITY: ATP + AMP -> ADP + ADP.
CC -1- SUBCELLULAR LOCATION: Mitochondrial.
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.

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CC EMBL: M77757; AAA34418.1; -
CC EMBL: X65126; CAA46254.1; -
CC EMBL: U18922; AAB64697.1; -
CC PIR: J01135; J01135.
CC PIR: S23568; S23568.
CC HSSP: P08760; ZAK3.
CC SGD: S0000972; ZAK2.
CC InterPro: IPR000850; Adenylate_kin.
CC Pfam: PF00406; adenylatekinase_1.
CC PRINTS: PR00094; ADENYLTKINASE.
CC ProDom: PD000657; Adenylate_kin. 1.
CC PROSITE: PS00113; ADENYLATE_KINASE. 1.
CC Transferase: kinase; ATP-binding; Mitochondrion.
CC NP_BIND 21 29 ATP (by SIMILARITY).
CC SEQUENCE 225 AA; 25194 MW; 3B192BE2535BF91F CRC64;

Query Match 37.9%; Score 439.5; DB 1; Length 225;
Best local Similarity 44.9%; Pred. No. 7e-31;
Matches 93; Conservative 37; Mismatches 66; Indels 11; Gaps 4;

QY 8 LRAVINGAPSGKGVSSRTTHF-ELKHLSSGDLRDNNLRGTEIGVLAKAFIDQGLI 66
DB 15 LRLLLGAPSGKGTOTSRLLKQIPOLSSISSDILRQEFKISSTGLGREATVYIAQKLL 74
QY 67 PDDVMTRLALHEKLN-----TOYSWLDGPPRLPQAEADRAYQ-----IDVYNLNP 117
DB 75 PDDLITRLTFRISALGWLKPSAMWLDGPPRTAQSALDELKQHDASLNLVLELDVP 134
QY 118 FEVTKORLFRWHPASGRVYNIEFPNPKTVGIDDLTGEPLDIOREDKPEPTVIRKLKAYE 177
DB 135 ESTILERIENKRYHVPSGRVYNQYNPVKPGDIDITGEPLTRDDTAEVFKRLREYK 194
QY 178 DQTKXVLYXYYQKKVLETSGETETNKI 204
DB 195 KTEPLKDYKKSGIFGTGSG-ETSDI 220

RESULT 12
KAD_ARATH STANDARD: PRT: 246 AA.

AC 082514; 09FPMW2;
DT 15-OCT-2001 (Rel. 40, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).
GN ADK1 OR ATSG63400 OR MLE2.3.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxId=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-cv. Columbia;
RA Weerts B., Thornburg R.;
RT "Characterization of the cDNA and gene for the Arabidopsis thaliana
RT adenylate kinase."
RL (in) Plant Gene Register PGR98-166.
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-cv. Columbia;
RX MEDLINE-98162728; PubMed-9501997;
RA Nakamura Y., Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. III.
RT Sequence features of the regions of 1,191,918 bp covered by seventeen
RT physically assigned pl. clones."
RL DNA Res. 4:401-414(1997).
CC -1- FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR
CC MAINTENANCE AND CELL GROWTH.
CC -1- CATALYTIC ACTIVITY: ATP + AMP -> ADP + ADP.
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
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CC EMBL: AF082882; AAC78478.1; -
CC EMBL: AB007649; BAB08805.1; -
CC HSSP: P07170; IAKY.
CC InterPro: IPR000850; Adenylate_kin.
CC Pfam: PF00406; adenylatekinase_1.
CC PRINTS: PR00094; ADENYLTKINASE.
CC ProDom: PD000657; Adenylate_kin. 1.
CC PROSITE: PS00113; ADENYLATE_KINASE. 1.

RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Ogell C.,
 RA Oliver P., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skellon J., Simmonds R., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volckaert G., Aert R., Robben J., Gymnopoulos B.,
 RA Woltens I., Vanstreets E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
 RA Bger P., Zimmermann W., Medler H., Wambolt R., Purnelle B.,
 RA Galteau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Gilbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe";
 RL Nature 415:871-880(2002).
 CC -1- FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR
 CC -1- MAINTENANCE AND CELL GROWTH.
 CC -1- CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.
 CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).

 DR EMBL: X70363; CAA49826.1; -;
 DR EMBL: Z69727; CAA83553.1; -;
 DR PIR: S31338; S31338.
 DR PIR: A46718; A46718.
 DR HSSP: P07170; IAKY.
 DR InterPro: IPR000850; Adenylate_kin.
 DR Pfam: PF00406; adenylatekinase; 1.
 DR PRINTS: PRO0094; ADENYLTKINASE.
 DR ProDom: PD000657; Adenylate_kin. 1.
 DR PROSITE: PS00113; ADENYLATE_KINASE; 1.
 DR K transferase; Kinase; ATP-binding.
 FT NP_BIND 10 18 ATP (BY SIMILARITY).
 FT SEQUENCE 220 AA; 24375 MW; F5335A025C971D78 CRC64;

 Query Match 37.6%; Score 436; DB 1; Length 220;
 Best Local Similarity 40.7%; Pred. No. 1.4e-30;
 Matches 87; Conservative 46; Mismatches 73; Indels 8; Gaps 3;

DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DE 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Adenylate kinase cytosolic (EC 2.7.4.3) (ATP-AMP transphosphorylase).
 GN AK1 OR AK11 OR AK1 OR AK12 OR YDR226W OR YD9934.11.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88194690; PubMed=2834097;
 RA Magdoen V., Oeschner U., Bandlow W.;
 RT "The complete nucleotide sequence of the gene coding for yeast
 RT adenylate kinase";
 RL Curr. Genet. 12:405-411(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88015563; PubMed=2821496;
 RA Proba K., Tomaselli A.G., Nielsen P., Schulz G.E.;
 RT "The cdna sequence encoding cytosolic adenylate kinase from baker's
 RT yeast (Saccharomyces cerevisiae).";
 RL Nucleic Acids Res. 15:7187-7187(1987).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89066766; PubMed=2848829;
 RA Konrad M.;
 RT "Analysis and in vivo disruption of the gene coding for adenylate
 RT kinase (ADK1) in the yeast Saccharomyces cerevisiae.";
 RL J. Biol. Chem. 263:19468-19474(1988).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95192063; PubMed=7885847;
 RA Davies C.J., Hutchison C.A. III;
 RT "Insertion site specificity of the transposon Tn3";
 RL Nucleic Acids Res. 23:507-514(1995).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=5288c / AB972;
 RA Murphy L., Harris D.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE OF 3-222.
 RX MEDLINE=86136113; PubMed=3004985;
 RA Tomaselli A.G., Mast E., Jones W., Schlitz E.;
 RT "The complete amino acid sequence of adenylate kinase from baker's
 RT yeast";
 RL Eur. J. Biochem. 155:111-119(1986).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (1.63 ANGSTROMS).
 RX MEDLINE=95400193; PubMed=7670369;
 RA Abele U., Schulz G.E.;
 RT "High-resolution structures of adenylate kinase from yeast ligated
 RT with inhibitor Ap5a, showing the pathway of phosphoryl transfer";
 RL Protein Sci. 4:1262-1271(1995).
 CC -1- FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR
 CC -1- MAINTENANCE AND CELL GROWTH.
 CC -1- CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
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 CC or send an email to license@sib-sib.ch).

 EMBL: M18455; AAA6319.1; -;
 DR EMBL: U13239; AAC33143.1; -;
 DR EMBL: Y00413; CAA68471.1; -;
 EMBL: X06304; CAA29624.1; -;

DR EMBL: Z48612; CAA88506.1; -
 DR PIR: S05799; KIBIA.
 DR PIR: S47934; S47934.
 DR PIR: S47475; S47475.
 DR PDB: 1AKY; 14-NOV-95.
 DR PDB: 2AKY; 14-NOV-95.
 DR PDB: 3AKY; 14-NOV-95.
 DR PDB: 1DVR; 03-APR-96.
 DR SWISS-2DPAGE; P07170; YEAST.
 DR SGD: S0002634; ADK1.
 DR InterPro: IPR000850; Adenylate_kin.
 DR pfam: PF00406; adenylatekinase; 1.
 DR PRINTS; PRO0094; ADENYLKINASE.
 DR PRODom; PD000657; Adenylate_kin; 1.
 DR PROSITE; PS00113; ADENYLATE_KINASE; 1.
 KW transferase; kinase; Acetylation; ATP-binding; 3D-structure.
 FT PROPEP 1 222 REMOVED IN MATURE FORM.
 FT CHAIN 3 222 ADENYLATE KINASE CYTOSOLIC.
 FT MOD_RES 3 3 ACETYLATION.
 FT NP_BIND 13 21 ATP (BY SIMILARITY).
 FT CONFLICT 139 139 A -> R (IN REF. 2).
 FT CONFLICT 222 222 D -> N (IN REF. 6).
 SQ SEQUENCE 222 AA; 24255 MW; FE566FD8015907CE CRC64;

Query Match 37.5%; Score 435; DB 1; Length 222;
 Best Local Similarity 40.3%; Pred. No. 1.7e-30;
 Matches 89; Conservative 50; Mismatches 72; Indels 10; Gaps 3;
 QY 3 ASARLLRAVYMGAPSGSGKGVSSRITTHPELKLHSSGDLIRDMMLGTEIGVLAFAFDQ 62
 Db 2 SSESIRWVLIGPPGAGKGTQAPNLOERFHAHLATGDMLSQIAKGTQGLGKAKIMDQ 61
 QY 63 GKLIIPDVMTRLALHELKN--LTQYSMLDGFEPRTLPQAEALDRAYQ----IDTVINLN 115
 Db 62 GGLVSDIDIVNMKIDELTNNPACKNGEILDGFERTIPQAEKLDQMKEGSTPLEKAIELK 121
 QY 116 VPPEVTKQRLTAMWHPASGRVYNIEFPNPKTVGIDDLTGEPLIQREDDKPTVIRKLA 175
 Db 122 VDDELVARITGRLIHPASGRSYHKIFNPKEDMKDDVTGEALVQSRSDNADALKRRLAA 181
 QY 176 YEDQTKXVLXYXOKGVLEFEGSTETNKIMPYVYAFLOTKV 216
 Db 182 YHAQTEPIVDFTKKTGI--WAGVDASOPPATWADILNKL 219

Search completed: March 19, 2003, 16:08:48
 Job time : 314 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 19, 2003, 15:45:51 ; Search time 272 seconds

(without alignments)
24.555 Million cell updates/sec

Title: US-10-006-190-1

Perfect score: 1161

Sequence: 1 MGASARLLRAVIMGAPGSGK.....VYAFIQTKVPGRSQKASVTP 227

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/protodata/1/1aa/5A_COMB.pep:*

2: /cgn2_6/protodata/1/1aa/5B_COMB.pep:*

3: /cgn2_6/protodata/1/1aa/5A_COMB.pep:*

4: /cgn2_6/protodata/1/1aa/5B_COMB.pep:*

5: /cgn2_6/protodata/1/1aa/5C_COMB.pep:*

6: /cgn2_6/protodata/1/1aa/5D_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1157	99.7	227	2	US-08-829-027-1
2	1157	99.7	227	3	US-09-225-366-1
3	1156	99.6	227	4	US-09-149-476-377
4	1091	94.0	227	2	US-08-829-027-3
5	1091	94.0	227	3	US-09-225-366-3
6	1038	89.4	227	2	US-08-829-027-4
7	1038	89.4	227	3	US-09-225-366-4
8	700.5	60.3	223	2	US-08-829-027-5
9	700.5	60.3	223	3	US-09-225-366-5
10	412.5	35.5	222	4	US-09-134-001C-3289
11	222.5	19.2	194	2	US-08-879-561-12
12	221	19.0	194	3	US-08-879-561-11
13	187	16.1	197	2	US-08-879-561-5
14	81	7.0	488	4	US-08-985-343-1
15	80.5	6.9	620	4	US-08-637-670-40
16	80.5	6.9	620	3	US-08-335-844A-24
17	78	6.7	373	4	US-09-071-035-116
18	78	6.7	406	4	US-09-071-035-114
19	76	6.5	531	4	US-08-687-590-29
20	76.5	6.6	284	4	US-09-134-001C-3329
21	76	6.5	397	4	US-09-134-001C-4188
22	76	6.5	1027	4	US-09-162-021B-2
23	75.5	6.5	464	4	US-09-134-001C-4562
24	74.5	6.4	335	4	US-08-987-146-2
25	74.5	6.4	419	4	US-09-120-426-2
26	73.5	6.3	898	1	US-08-036-210-22
27	73.5	6.3	898	2	US-08-449-609-22

28	73	6.3	408	2	US-08-683-007A-2	Sequence 2, Appl1
29	73	6.3	600	4	US-09-134-001C-3636	Sequence 3636, Ap
30	72.5	6.2	296	1	US-08-241-465B-21	Sequence 21, Appl
31	72.5	6.2	491	3	US-08-923-454A-14	Sequence 14, Appl
32	72.5	6.2	820	1	US-08-166-717D-6	Sequence 6, Appl1
33	72	6.2	229	4	US-09-134-001C-4113	Sequence 4113, Ap
34	72	6.2	303	2	US-08-321-670-2	Sequence 2, Appl1
35	72	6.2	303	4	US-09-215-252-3	Sequence 3, Appl1
36	71.5	6.2	1663	2	US-08-793-126-1	Sequence 1, Appl1
37	71.5	6.2	1663	4	US-09-132-271-1	Sequence 2, Appl1
38	71.5	6.2	1663	4	US-09-142-334-22	Sequence 23, Appl
39	71.5	6.2	2089	1	US-08-418-893D-23	Sequence 24, Appl
40	71.5	6.2	2089	1	US-08-418-893D-24	Sequence 21, Appl
41	70.5	6.1	408	1	US-07-951-715A-21	Sequence 21, Appl
42	70.5	6.1	408	2	US-08-459-448A-21	Sequence 21, Appl
43	70.5	6.1	408	3	US-08-459-595A-21	Sequence 21, Appl
44	70.5	6.1	408	3	US-08-459-504B-21	Sequence 21, Appl
45	70.5	6.1	408	3	US-08-459-444-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-08-829-027-1
; Sequence 1, Application US/08829027
; Patent No. 5856160
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,027
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0256 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Consensus
; CLONE: 2122022
; US-08-829-027-1
Query Match 99.7%; Score 1157; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 4.3e-129;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGASARLLRAVIMGAPGSGKTVSSRITTHPELKLHSSGDLRDNNLRGTEIGVLAKAFI 60
Db 1 MGASARLLRAVIMGAPGSGKTVSSRITTHPELKLHSSGDLRDNNLRGTEIGVLAKAFI 60
Qy 61 DOGKLIPDDVMTRLALHELNLTQYSMLLDGFPRTLPOAEALDRAVOIDTVINLNVPEV 120
Db 61 DOGKLIPDDVMTRLALHELNLTQYSMLLDGFPRTLPOAEALDRAVOIDTVINLNVPEV 120
Qy 121 IKORLTARMIHPASGRVNIIEFNPPKTVGIDDLTGEPILQREDKPEYIKRLKAYEDOT 180
Db 121 IKORLTARMIHPASGRVNIIEFNPPKTVGIDDLTGEPILQREDKPEYIKRLKAYEDOT 180
Qy 181 KXVLXYOKKGVLETFSGTETNKIMPYVYAFLOTKVPQRSOKASVTP 227
Db 181 KXVLXYOKKGVLETFSGTETNKIMPYVYAFLOTKVPQRSOKASVTP 227

RESULT 2

US-09-225-366-1
Sequence 1, Application US/09225366
Patent No. 6001624
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,366
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/829,027
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: Pf-0256 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Consensus
CLONE: 2122022
US-09-225-366-1

Query Match

Best Local Similarity 99.7%; Score 1157; DB 3; Length 227;
Pred. No. 4,3e-129;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MGASARLLRAVIMGAPGSGKTVSSRITTHPELKLHSSGDLRDNNLRGTEIGVLAKAFI 60

Qy 61 DOGKLIPDDVMTRLALHELNLTQYSMLLDGFPRTLPOAEALDRAVOIDTVINLNVPEV 120
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Qy 121 IKORLTARMIHPASGRVNIIEFNPPKTVGIDDLTGEPILQREDKPEYIKRLKAYEDOT 180
Db 121 IKORLTARMIHPASGRVNIIEFNPPKTVGIDDLTGEPILQREDKPEYIKRLKAYEDOT 180
Qy 181 KXVLXYOKKGVLETFSGTETNKIMPYVYAFLOTKVPQRSOKASVTP 227
Db 181 KXVLXYOKKGVLETFSGTETNKIMPYVYAFLOTKVPQRSOKASVTP 227

RESULT 3

US-09-149-476-377
Sequence 377, Application US/09149476
Patent No. 6420526
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002p1
CURRENT APPLICATION NUMBER: US/09/149,476
EARLIER FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07
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EARLIER APPLICATION NUMBER: 60/040,334
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,336
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,163
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/047,600
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,615
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,597
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,502
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EARLIER APPLICATION NUMBER: 60/047,592
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EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,598
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EARLIER APPLICATION NUMBER: 60/047,613
EARLIER FILING DATE: 1997-05-23

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EARLIER APPLICATION NUMBER: 60/047,632
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,601
EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,568
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,314
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EARLIER APPLICATION NUMBER: 60/043,569
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EARLIER APPLICATION NUMBER: 60/056,886
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,877
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,889
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,893
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,630
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,878
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,662
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,872
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,882
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,637
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,903
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,888
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,879
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,880
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,894
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,911
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,636
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,874
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,910

EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,864
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,631
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,845
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,892
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,761
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/047,595
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,599
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,588
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,585
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,586
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,590
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,594
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,589
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,593
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,614
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,578
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,876
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,881
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,909
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,875
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02

Query Match 99.6% Score 1156: DB 4: Length 227:
Best Local Similarity 99.1% Pred. No. 5.7e-129;
Matches 225; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGASARLLRAVIMGAPGSGKTVSSRITTHFELKHLSSGDLRDNMRLKGTETIGVLAKEFI 60
DB 1 MGASARLLRAVIMGAPGSGKTVSSRITTHFELKHLSSGDLRDNMRLKGTETIGVLAKEFI 60
QY 61 DOGKLIIPDDVMTRLALHELNLTQYSWLLDGFPRRLPOAEALDRAYQIDVTYNLNVPEV 120
DB 61 DOGKLIIPDDVMTRLALHELNLTQYSWLLDGFPRRLPOAEALDRAYQIDVTYNLNVPEV 120
QY 121 IKQRLTARWIHPASGRVYNIENPPKTVGIDDLTGEPLIQREDDKPEYIKRLKAYEODT 180
DB 121 IKQRLTARWIHPASGRVYNIENPPKTVGIDDLTGEPLIQREDDKPEYIKRLKAYEODT 180
QY 181 KXVLXYOKKGVLETFSGTETNKIMPYVYAFLOTKVPQSRKASYTP 227
DB 181 KXVLXYOKKGVLETFSGTETNKIMPYVYAFLOTKVPQSRKASYTP 227

RESULT 4
US-08-829-027-3

; Sequence 3, Application US/08829027
; Patent No. 5856160
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESS: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,027
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0256 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Genbank
; CLONE: 217576
US-08-829-027-3

Query Match 94.0%; Score 1091; DB 2; length 227;

Best Local Similarity 91.6%; Pred. No. 3e-121;
Matches 208; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 MGASARLLRAVIMGAPGSGKTVSSRITTHFELKHLSSGDLRDNMRLKGTETIGVLAKEFI 60
DB 1 MGASARLLRAVIMGAPGSGKTVSSRITTHFELKHLSSGDLRDNMRLKGTETIGVLAKEFI 60

QY 61 DOGKLIIPDDVMTRLALHELNLTQYSWLLDGFPRRLPOAEALDRAYQIDVTYNLNVPEV 120
DB 61 DOGKLIIPDDVMTRLALHELNLTQYSWLLDGFPRRLPOAEALDRAYQIDVTYNLNVPEV 120
QY 121 IKQRLTARWIHPASGRVYNIENPPKTVGIDDLTGEPLIQREDDKPEYIKRLKAYEODT 180
DB 121 IKQRLTARWIHPASGRVYNIENPPKTVGIDDLTGEPLIQREDDKPEYIKRLKAYEODT 180
QY 181 KXVLXYOKKGVLETFSGTETNKIMPYVYAFLOTKVPQSRKASYTP 227
DB 181 KXVLXYOKKGVLETFSGTETNKIMPYVYAFLOTKVPQSRKASYTP 227

RESULT 5
US-09-225-366-3

; Sequence 3, Application US/09225366
; Patent No. 6001624
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESS: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,366
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/829,027
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0256 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Genbank
; CLONE: 217576
US-09-225-366-3

Query Match 94.0%; Score 1091; DB 3; length 227;

Best Local Similarity 91.6%; Pred. No. 3e-121;
Matches 208; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 MGASARLLRAVIMGAPGSGKTVSSRITTHFELKHLSSGDLRDNMRLKGTETIGVLAKEFI 60
DB 1 MGASARLLRAVIMGAPGSGKTVSSRITTHFELKHLSSGDLRDNMRLKGTETIGVLAKEFI 60
QY 61 DOGKLIIPDDVMTRLALHELNLTQYSWLLDGFPRRLPOAEALDRAYQIDVTYNLNVPEV 120
DB 61 DOGKLIIPDDVMTRLALHELNLTQYSWLLDGFPRRLPOAEALDRAYQIDVTYNLNVPEV 120
QY 121 IKQRLTARWIHPASGRVYNIENPPKTVGIDDLTGEPLIQREDDKPEYIKRLKAYEODT 180
DB 121 IKQRLTARWIHPASGRVYNIENPPKTVGIDDLTGEPLIQREDDKPEYIKRLKAYEODT 180

Db 121 IKORLTARWHPASGRVYNIENFNPCKTGMGIDDLTGEPLVQREDRPEVTYKRLKAYEAO 180

QY 181 KXVLXYQKKGVLETFSGTETNKIMPYVYAFLOTKVPORSOKASVTP 227
Db 181 EPLVLEYQKKGVLETFSGTETNKIMPHYVAFLOTKLPORSOETSIVTP 227

RESULT 6

US-08-829-027-4
Sequence 4, Application US/08829027
Patent No. 5856160
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: IBM Compatible
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/829,027
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0256 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 450312
US-08-829-027-4

Query Match 89.4%; Score 1038; DB 2; Length 227;
Best Local Similarity 90.3%; Pred. No. 5.8e-115;
Matches 205; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 1 MGASARLLRAVIMGAPSGKGVSSRTTTFHELKHLSSGDLRDNMLRGTEIGVLAFAFI 60
Db 1 MGASGRLLRAVIMGAPSGKGVSSRTTTFHELKHLSSGDLRDNMLRGTEIGVLAFAFI 60
QY 61 DQGLIPDDVMTRLALHELKLNLTQYSWLDDGFPTLPQAEALDRAVOIDTVINLVNPFV 120
Db 61 DQGLIPDDVMTRLALHELKLNLTQYSWLDDGFPTLPQAEALDRAVOIDTVINLVNPFV 120
QY 121 IKORLTARWHPASGRVYNIENFNPCKTVGIDDLTGEPLIQREDKPEVTYKRLKAYEDOT 180
Db 121 IKRLTARWHPASGRVYNIENFNPCKTVGIDDLTGEPLIQREDKPEVTYKRLKAYEAO 180
QY 181 KXVLXYQKKGVLETFSGTETNKIMPYVYAFLOTKVPORSOKASVTP 227
Db 181 EPLVLEYQKKGVLETFSGTETNKIMPHYVAFLOTKLPORSOETSIVTP 227

Db 181 EPLVLEYQKKGVLETFSGTETNKIRPHYVSFLQKKVPEITQKASVTP 227

RESULT 7
US-09-225-366-4
Sequence 4, Application US/09225366
Patent No. 6001624

GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: IBM Compatible
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,366
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/829,027
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0256 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 450312
US-09-225-366-4

Query Match 89.4%; Score 1038; DB 3; Length 227;
Best Local Similarity 90.3%; Pred. No. 5.8e-115;
Matches 205; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 1 MGASARLLRAVIMGAPSGKGVSSRTTTFHELKHLSSGDLRDNMLRGTEIGVLAFAFI 60
Db 1 MGASGRLLRAVIMGAPSGKGVSSRTTTFHELKHLSSGDLRDNMLRGTEIGVLAFAFI 60
QY 61 DQGLIPDDVMTRLALHELKLNLTQYSWLDDGFPTLPQAEALDRAVOIDTVINLVNPFV 120
Db 61 DQGLIPDDVMTRLALHELKLNLTQYSWLDDGFPTLPQAEALDRAVOIDTVINLVNPFV 120
QY 121 IKORLTARWHPASGRVYNIENFNPCKTVGIDDLTGEPLIQREDKPEVTYKRLKAYEDOT 180
Db 121 IKRLTARWHPASGRVYNIENFNPCKTVGIDDLTGEPLIQREDKPEVTYKRLKAYEAO 180
QY 181 KXVLXYQKKGVLETFSGTETNKIMPYVYAFLOTKVPORSOKASVTP 227
Db 181 EPLVLEYQKKGVLETFSGTETNKIRPHYVSFLQKKVPEITQKASVTP 227

RESULT 8
US-08-829-027-5

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Sequence 5, Application US/08829027
Patent No. 5856160
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/829,027
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0256 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 28577
US-08-829-027-5

Query Match 60.3%; Score 700.5; DB 2; Length 223;
Best Local Similarity 58.8%; Pred. No. 6,4e-75;
Matches 130; Conservative 38; Mismatches 52; Indels 1; Gaps 1;

QY 4 SARLLRAVIMGAPGSGKTVSSRTTHFELKHLSSGDLRLDMMLRGTEIGVLA KAFIDG 63
DB 2 ASKLLRAVILGPPGSGKTVCCORINQNFGLQHLSSGHFLRENKASTEGEMAKQIYES 61
QY 64 KLIPDDVMTRLALHLEKLNLTQYSWLLDGPRTLPOAEALDRAYQIDTVINLVPEVIKQ 123
DB 62 LVPDPIVITRLMSELENRGQHWLLDGPRTLGOAEALDKICEVDLVISLNIPEETLKD 121
QY 124 RLTAARHHPASGRVYNIEFNPKVTGIDDLTGEPLIQREDDKPEYVIRKLA YEQTKYV 183
DB 122 RLSRMRHPPSGRVYNLDENPPHVHGIDVTGEPLVQOEDDKPEVAARLRQYKQVAKFV 181
QY 184 LXYOKKGVLTFETSGTETNKIMPYVYAFLOTQKV-PORSOKA 223
DB 182 IELYKSRGVLHQFSGTETNKIMPYVYTLFSNKITPIQSKEA 222

RESULT 9
US-09-225-366-5
Sequence 5, Application US/09225366
Patent No. 6001624
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
```

```
TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,366
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/829,027
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0256 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 28577
US-09-225-366-5

Query Match 60.3%; Score 700.5; DB 3; Length 223;
Best Local Similarity 58.8%; Pred. No. 6,4e-75;
Matches 130; Conservative 38; Mismatches 52; Indels 1; Gaps 1;

QY 4 SARLLRAVIMGAPGSGKTVSSRTTHFELKHLSSGDLRLDMMLRGTEIGVLA KAFIDG 63
DB 2 ASKLLRAVILGPPGSGKTVCCORINQNFGLQHLSSGHFLRENKASTEGEMAKQIYES 61
QY 64 KLIPDDVMTRLALHLEKLNLTQYSWLLDGPRTLPOAEALDRAYQIDTVINLVPEVIKQ 123
DB 62 LVPDPIVITRLMSELENRGQHWLLDGPRTLGOAEALDKICEVDLVISLNIPEETLKD 121
QY 124 RLTAARHHPASGRVYNIEFNPKVTGIDDLTGEPLIQREDDKPEYVIRKLA YEQTKYV 183
DB 122 RLSRMRHPPSGRVYNLDENPPHVHGIDVTGEPLVQOEDDKPEVAARLRQYKQVAKFV 181
QY 184 LXYOKKGVLTFETSGTETNKIMPYVYAFLOTQKV-PORSOKA 223
DB 182 IELYKSRGVLHQFSGTETNKIMPYVYTLFSNKITPIQSKEA 222

RESULT 10
US-09-134-001C-3289
Sequence 3289, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1996-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
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? PRIOR FILING DATE: 1997-11-08
? PRIOR APPLICATION NUMBER: US 60/055,779
? PRIOR FILING DATE: 1997-08-14
? NUMBER OF SEO ID NOS: 5674
? SEO ID NO 3789
? LENGTH: 222
? TYPE: PRT
? ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3289

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Query Match	35.5%	Score 412.5;	DB 4;	Length 222;
Best Local Similarity	41.3%;	Pred. NO. 9.7e-41;		
Matches 86; Conservative	41;	Mismatches 70;	Indels 11;	Gaps 3

QY	8	LRAVIMAPGSGKCTVSSRITTHELKHLSGDLRLNMTGRTIGVLAAFIIDQGLIP	67
	:	::: : : : : : : : : : : : : :	
Db	8	MNIIIMLPGAGKCTQASLKYKRPPIHISIGDMFKRAIKDEIDUGKEMSNDRGELVP	67
QY	68	DDVMTRLALHEL-KNLQYSWLDDGFPRTLPQAEALDRAY-----QIDTVINLNVPEVI	121
	:	: : : : : : : : : : : : : :	
Db	68	DEVTVGIYKERISDDDAKKGLDGGFPRTIDQAEASLNGINSELDREIDAVINIEVPEEL	122
QY	122	KQRLTARINHASGRVYNIEFNPKYTVGIDDLTGEPPLQREDDKPEFVYIKRLAKAYEDQTK	181
	:	: : : : : : : : : : : : : :	
Db	128	MNRLTGRIKCEKCTTYHVLNPNPKVGVGICIDIDEGCKLYOREDDNPETVSNRLSYVNRQSK	187
QY	182	XVLXYOKKGVLETFESGTE-----TNKI	204
Db	188	PILEYINNKGVALKNIDSGKQIDDEVYTNQV	215

RESULT 11
US-08-879-561-12
; Sequence 12, Application US/08879561
; Patent No. 5817487

1 GENERAL INFORMATION:
 2 APPLICANT: Bandman, Olga
 3 APPLICANT: Hillman, Jennifer L.
 4 APPLICANT: Hawkins, Phillip R.
 5 APPLICANT: Guegler, Karl J.
 6 APPLICANT: Corley, Neil C.
 7 TITLE OF INVENTION: DISEASE RELATED NUCLEOTIDE KINASEE
 8 NUMBER OF SEQUENCES: 12
 9 CORRESPONDENCE ADDRESS:
 10 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 11 STREET: 3174 Porter Drive
 12 CITY: Palo Alto

```

1  COMPUTER READABLE FORM:
2  MEDIUM TYPE: Diskette
3  COMPUTER: IBM Compatible
4  OPERATING SYSTEM: DOS
5  SOFTWARE: FastSEO for Windows Version 2.0
6  CURRENT APPLICATION DATA:
7  APPLICATION NUMBER: US/08/879,561

```

ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0325 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 194 amino acids

```

;      TYPE: amino acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
US-08-879-561-12

```

Query Match	19.28;	Score 222.5;	DB 2;	Length 194;
Best Local Similarity	28.38;	Pred. No. 2.8e-18;		
Matches 58; Conservative	44;	Mismatches 72;	Indels 31;	Gaps 5,

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0Y      72  TRLALHEL--KNLTQYMWLDGEPRTLQAEALDRAVOIDT-VINLVNPREVIKORTLAR 128B
Db      14  VVGGRSGSGKGQCKEYHNKKGYTHLSVGDLLRAEYSSSGSEKGLQAIIMEKGEVLPLVDIV 73
0Y      12  IMGAPSGSGKGVSSRIITTHELKLSSGDDLNDMLMGTETGVLAKAFIDQGIKLPDVM 71
Db      14  VVGGRSGSGKGQCKEYHNKKGYTHLSVGDLLRAEYSSSGSEKGLQAIIMEKGEVLPLVDIV 73
0Y      74  LDMRLDAMLAKADTSKSGFLIDGYPREYKQSGEEFEKKIAPPTLLLYVDAGKETWYKRLIKR 133B
Db      129 WIHPSGRVRYVNIERNPPKVTGIDVLJGEBPLQRERDOKPEYVIKRLAYEBOQTKVLLXYQ 168B
Db      134 --GETSGV-----DDEEETIKKLEIYYVAKATEPVIAFYK 166B
0Y      189 KKGVLTEFSGFET-NKIMPYVYAEFL 212
Db      167 GRGIYROLNAGETVDEYFQOVCSTL 191

```

RESULT 12
US-08-879-561-11
; Sequence 11, Application US/08879561

GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: DISEASE RELATED NUCLEOTIDE KINASES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA

```

1  COMPUTER READABLE FORM:
2  MEDIUM TYPE: Diskette
3  COMPUTER: IBM Compatible
4  OPERATING SYSTEM: DOS
5  SOFTWARE: FAST-SEO for Windows Version 2.0
6  CURRENT APPLICATION DATA:
7  APPLICATION NUMBER: US/08/879, 561

```

ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0325 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:

```

: INFORMATION FOR SEQ ID NO: 11:
:
: SEQUENCE CHARACTERISTICS:
:
:   LENGTH: 194 amino acids
:
:   TYPE: amino acid
:
: STRADEDNESS: single
:
: TOPOLOGY: linear
:
:
: US-08-879-561-11

```

RESULT 13
US-08-879-561-5
; Sequence 5, Application US/08879561
; Data# No 5017403

	Matches	57;	Conservative	32;	Mismatches	60;	Indels	56;	Gaps	7;
OY	12	IMGAGSGSGKGYSSKITT	FEELKHSSGDLNDNMRGEIVGAKAFIDOGKILPDDVM	71						
		:	: :	: :	: :	: :	: :	: :		
Db	16	IIGGGSGSGKGYTCEKLE	VEKGYFTHTSTGLREELASEBSERKLLIRDIMERDGLVPSGIV	75						
OY	72	TRLALHEKLNLTQYS---	WLDGFPPTLRQAEALDAVQIDTVINLNVPEFVIRKRL	125						
			: :	: :	: :	: :		: :		
Db	76	LEL-----LKEANVA	SLGIDTRGLIDGYPREVAQGEFGR-----RIGDPQLVYIMCQ	123						
OY	126	TARWTHPASGRVYNLE	NPPTKVGIDDLTGEPLIORE-----DDKPETVIRKLAYEDQ	179						
			: :	: :	: :	: :	: :	: :		
Db	124	SA-----	DTMTNR-LIORSRSSLPVDDTTKIARLRLAAYRA	159						
OY	180	TKXVLXYYOKKGVL	ETFGSTENKI	204						
		: : : :	: :	: :	: :	: :	: :	: :		
Db	160	SIPVIAAYETK-----	TOLHKT	176						

RESULT 14
US-08-985-343-1
; Sequence 1, Application US/08985343
; Patent No. 6468782

```

APPLICANT: Tunnaciff, Alan G.
APPLICANT: Welsh, David T.
APPLICANT: Roser, Bruce J.
APPLICANT: Dhaliwal, Kamaljit S.
APPLICANT: Colaco, Camilo
TITLE OF INVENTION: METHODS OF PRESERVING PROKARYOTIC CELLS
TITLE OF INVENTION: AND COMPOSITIONS OBTAINED THEREBY
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,343
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 26374-20017.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141 MRSNDRS SRO
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-985-343-1

```

Query Match	7.08; Score 81; DB 4; Length 488;
-------------	-----------------------------------

Matches	48;	Conservative	20;	Mismatches	60;	Indels	70;	Gaps	11;
---------	-----	--------------	-----	------------	-----	--------	-----	------	-----

```

QY      65 LIPDWTATRLALHKLKLVQYSML-DGPF-----RLPPAE-----100
      111: 1: :111: 1 11 111:
Db      161 LIPMIRQIVAKKLKNI-KIGWFLHTPPSSSEYIRILPVQELIKVLSCDLIGFTYD 219
QY      101 -----ALDRAVIDIVLNLPFEVIKQRLTARKMTHPMSGRYNIENPPKTVGIDDL 153

```

```
Db 220 YAHFLSAVORILNVTLPN-GVEFD-----GRFVWGAFP---IGIDVE 260
QY 154 TGEPLIQREDDKPEYVIKRIKAKVEDQTKV-----LXYT---QKGVLETFEGTET 201
Db 261 T-----FTBGLKODAVIKRIKESFKCKGKIIIGVDRLDYIKGVPOKHLALEVFLGAHP 315
QY 202 NKIMPVYVAFLQTKVPOR 219
Db 316 E--WICKVVLQVAVPSR 331
```

RESULT 15

```
US-08-637-670-40
; Sequence 40, Application US/08637670
; Patent No. 6413521
;
; GENERAL INFORMATION:
; APPLICANT: MCMICHAEL-PHILLIPS et al.
; TITLE OF INVENTION: Helminth Parasite Antigen with
; TITLE OF INVENTION: Aminopeptidase-like Activity
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Barbara G. Ernst
; STREET: 555 13TH STREET, NW Suite 701E
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/637,670
; FILING DATE: 26-JUN-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Ernst, Barbara G.
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1811-0232
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 620 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-637-670-40
```

Query Match 6.9%: Score 80.5; DB 4; Length 620;

Best Local Similarity 23.8%: Pred. No. 1.2; Mismatches 54; Indels 71; Gaps 11;

```
Matches 46; Conservative 22;
QY 25 SRTTHPELKHLSGDL-----LRDNMLRGTEIGVLAFAIDQKLIIPDDVWTRL 74
Db 35 ARIVAH-ELAHQWFGDLVTKMKWDNLNMGFAFTE-----FIGAGQITQDDAMR- 85
QY 75 ALHELKLNLOYSWLIDGFPRTLPAQALDRAIYIDVINLNVPPEVIKQRLTARWIHPAS 134
Db 86 -----NY-FLID-----VLERALKADSVAS-----SHPLS 109
QY 135 GRVYNIEFPNPPTVGIDDLTGEPPLIQREDDKPEYVIKRIKAY--EDQTKXVLYYQKGV 192
Db 110 ---FRIDKAAVEAEAFDDITYA-----KGASVLTMLRALIGEEKHHAASQYLRK-- 156
QY 193 LETFSGTETNKIW 205
Db 157 -FSYSNAEATDLW 168
```

Search completed: March 19, 2003, 16:49:22
Job time : 277 secs

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XX WPI: 1998-557119/47.
DR N-PSDB: AAV68223.
XX
XX Human mitochondrial adenylate kinase, HMAK - useful e.g. to treat
PT neurological disorders such as Alzheimer's and screen for
PT antagonists for treatment of cancer or immunological disorders
XX
XX Claim 5; Fig 1; 63pp; English.
XX
CC The human mitochondrial adenylate kinase (HMAK) protein of 227 amino
CC acids) can be administered therapeutically, especially by expressing
CC encoding polypeptides, to treat neurological disorders e.g. Alzheimer's
CC disease, Huntington's disease, epilepsy. It can be combined with a
CC suitable carrier in pharmaceutical compositions, which can be
CC administered to treat such disorders. HMAK was shown to have chemical
CC and structural homology with adenylate kinase isozyme 3 (AK3) from cow,
CC rat and human (92, 91 and 57 % identity respectively) and was expressed
CC in e.g. cancerous tissues, brain and neural tissues and tissues involved
CC in inflammation and the immune response. Increased activity or
CC expression was proposed to be associated with cancer and immunological
CC disorders, and decreased activity/expression with the development of
CC neurological disorders. Products of the above invention may be used in
CC the diagnosis and treatment of the above diseases and disorders.
XX
SQ Sequence 227 AA:

Query Match 99.7%; Score 1157; DB 19: Length 227;
Best Local Similarity 100.0%; Pred. No. 2.1e-111;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGASARLLRAVIMGAPGSGKTGVSRRITTHFEIKHLSSGDLRLDNLKRGTEIGVLAKAT 60
DB 1 MGASARLLRAVIMGAPGSGKTGVSRRITTHFEIKHLSSGDLRLDNLKRGTEIGVLAKAT 60
QY 61 DGGKLLPDVWTRRLAHEKNTQYSWLDGFRRLPOAEALDRAYOIDTVINLVNPFV 120
DB 61 DGGKLLPDVWTRRLAHEKNTQYSWLDGFRRLPOAEALDRAYOIDTVINLVNPFV 120
QY 121 IKQRLTARMIHPASGRVYIEFNPPKTVGIDDLTGEPRLQREDDKPEYIKRLKAYEDPT 180
DB 121 IKQRLTARMIHPASGRVYIEFNPPKTVGIDDLTGEPRLQREDDKPEYIKRLKAYEDPT 180
QY 181 KXVLXYQKKGVLFTFSGTETNKIMPYVYAFLOTKVPORSQKASYTP 227
DB 181 KXVLXYQKKGVLFTFSGTETNKIMPYVYAFLOTKVPORSQKASYTP 227

RESULT 2
AAW74787
ID AAW74787 standard; Protein; 227 AA.
AC AAW74787;
XX
XX 19-JAN-1999 (first entry)
DT
XX
XX Human secreted protein encoded by gene 58 clone HHFHN61.
DE
XX
KW Human: secreted protein; testis; tumour; foetal brain tissue;
KW fusion protein; cancer; central nervous system; seizure;
KW diagnosis; neurodegenerative disease.
XX
OS Homo sapiens.
XX
XX
PN MO9839448-A2.
XX
PD 11-SEP-1998.
XX
PF 06-MAR-1998; 98WO-US04493.
XX
XX 02-OCT-1997; 97US-0061060.
PR 07-MAR-1997; 97US-0038621.
PR 07-MAR-1997; 97US-0040161.
PR

PR 07-MAR-1997; 97US-0040162.
PR 07-MAR-1997; 97US-0040163.
PR 07-MAR-1997; 97US-0040333.
PR 07-MAR-1997; 97US-0040334.
PR 07-MAR-1997; 97US-0040336.
PR 07-MAR-1997; 97US-0040626.
PR 11-APR-1997; 97US-0043311.
PR 11-APR-1997; 97US-0043312.
PR 11-APR-1997; 97US-0043313.
PR 11-APR-1997; 97US-0043314.
PR 11-APR-1997; 97US-0043568.
PR 11-APR-1997; 97US-0043569.
PR 11-APR-1997; 97US-0043576.
PR 11-APR-1997; 97US-0043578.
PR 11-APR-1997; 97US-0043580.
PR 11-APR-1997; 97US-0043669.
PR 11-APR-1997; 97US-0043670.
PR 11-APR-1997; 97US-0043671.
PR 11-APR-1997; 97US-0043672.
PR 11-APR-1997; 97US-0043674.
PR 23-MAY-1997; 97US-0047492.
PR 23-MAY-1997; 97US-0047500.
PR 23-MAY-1997; 97US-0047501.
PR 23-MAY-1997; 97US-0047502.
PR 23-MAY-1997; 97US-0047503.
PR 23-MAY-1997; 97US-0047581.
PR 23-MAY-1997; 97US-0047582.
PR 23-MAY-1997; 97US-0047583.
PR 23-MAY-1997; 97US-0047584.
PR 23-MAY-1997; 97US-0047585.
PR 23-MAY-1997; 97US-0047586.
PR 23-MAY-1997; 97US-0047587.
PR 23-MAY-1997; 97US-0047588.
PR 23-MAY-1997; 97US-0047589.
PR 23-MAY-1997; 97US-0047590.
PR 23-MAY-1997; 97US-0047592.
PR 23-MAY-1997; 97US-0047593.
PR 23-MAY-1997; 97US-0047594.
PR 23-MAY-1997; 97US-0047595.
PR 23-MAY-1997; 97US-0047596.
PR 23-MAY-1997; 97US-0047597.
PR 23-MAY-1997; 97US-0047598.
PR 23-MAY-1997; 97US-0047599.
PR 23-MAY-1997; 97US-0047600.
PR 23-MAY-1997; 97US-0047601.
PR 23-MAY-1997; 97US-0047612.
PR 23-MAY-1997; 97US-0047613.
PR 23-MAY-1997; 97US-0047614.
PR 23-MAY-1997; 97US-0047615.
PR 23-MAY-1997; 97US-0047617.
PR 23-MAY-1997; 97US-0047618.
PR 23-MAY-1997; 97US-0047632.
PR 23-MAY-1997; 97US-0047633.
PR 06-JUN-1997; 97US-0048964.
PR 06-JUN-1997; 97US-0048974.
PR 13-JUN-1997; 97US-0049610.
PR 08-JUL-1997; 97US-0051926.
PR 16-JUL-1997; 97US-0052874.
PR 18-AUG-1997; 97US-0053724.
PR 22-AUG-1997; 97US-0056630.
PR 22-AUG-1997; 97US-0056631.
PR 22-AUG-1997; 97US-0056632.
PR 22-AUG-1997; 97US-0056636.
PR 22-AUG-1997; 97US-0056637.
PR 22-AUG-1997; 97US-0056662.
PR 22-AUG-1997; 97US-0056664.
PR 22-AUG-1997; 97US-0056845.
PR 22-AUG-1997; 97US-0056862.
PR 22-AUG-1997; 97US-0056864.
PR 22-AUG-1997; 97US-0056872.
PR 22-AUG-1997; 97US-0056874.
PR 22-AUG-1997; 97US-0056875.
PR 22-AUG-1997; 97US-0056876.

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PR 22-AUG-1997; 97US-0056877.
PR 22-AUG-1997; 97US-0056878.
PR 22-AUG-1997; 97US-0056879.
PR 22-AUG-1997; 97US-0056880.
PR 22-AUG-1997; 97US-0056881.
PR 22-AUG-1997; 97US-0056882.
PR 22-AUG-1997; 97US-0056884.
PR 22-AUG-1997; 97US-0056886.
PR 22-AUG-1997; 97US-0056887.
PR 22-AUG-1997; 97US-0056888.
PR 22-AUG-1997; 97US-0056889.
PR 22-AUG-1997; 97US-0056892.
PR 22-AUG-1997; 97US-0056893.
PR 22-AUG-1997; 97US-0056894.
PR 22-AUG-1997; 97US-0056903.
PR 22-AUG-1997; 97US-0056908.
PR 22-AUG-1997; 97US-0056909.
PR 22-AUG-1997; 97US-0056910.
PR 22-AUG-1997; 97US-0056911.
PR 05-SEP-1997; 97US-0057650.
PR 05-SEP-1997; 97US-0057659.
PR 05-SEP-1997; 97US-0057761.
PR 12-SEP-1997; 97US-0058785.
XX
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA;
PI Feng P, Ferrie AM, Fischer CL, Florence KA, Greene JM, Hu JS;
PI Kyaw H, Latleur DM, Li Y, Moore PA, Nl J, Olsen HS, Rosen CA;
PI Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
XX
XX WPI: 1998-506364/43.
XX N-PSDB: AAV59568.
XX
XX New isolated human genes and the secreted polypeptide(s) they encode
XX - useful for diagnosis and treatment of e.g. cancers, neurological
XX disorders, immune diseases, inflammation or blood disorders
XX
XX Claim 1: Page 575-576; 721pp; English.
XX
XX This sequence represents a secreted human protein encoded by the nucleic
XX acid molecule designated Gene 58 from the human cDNA clone HHPHN61
XX CC (deposited as clone ATCC 97899 and ATCC 209045).
XX CC The gene can be used to generate fusion proteins by linking to the gene
XX CC to a human immunoglobulin Fc portion (e.g. AAV59502) for increasing the
XX CC stability of the fused protein as compared to the human protein only.
XX CC The invention relates to 186 novel genes and their fragments (nucleic
XX CC acid sequences: AAV59511-V59612; amino acid sequences AAW4731-W5026)
XX CC which are useful for preventing, treating or ameliorating medical
XX CC conditions e.g. by protein or gene therapy. Also, pathological
XX CC polypeptides in a sample or by determining the amount of the new
XX CC the new polynucleotides. Specific uses are described for each of the 186
XX CC polynucleotides, based on which tissues they are most highly expressed in
XX CC (see AAV59511 for described uses).
XX
XX Sequence 227 AA:
SQ
Query Match 99.6%; Score 1156; DB 19; Length 227;
Best Local Similarity 99.1%; Pred. No. 2,7e-111;
Matches 225; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY 181 KYVLXYOKKKVLETFSGTEFNKIWPYVAFLQTKVPORSOKASVTP 227
DB 181 KPVLEYOKKKVLETFSGTEFNKIWPYVAFLQTKVPORSOKASVTP 227
RESULT 3
AAM38899 standard; Protein; 227 AA.
ID AAM38899
XX
XX AAM38899;
XX
XX 22-OCT-2001 (first entry)
XX
XX Human polypeptide SEQ ID NO 2044.
XX
XX Human; neotropic; immunosuppressant; cytostatic; gene therapy; cancer;
XX peripheral nervous system; neuropathy; central nervous system; CNS;
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
XX chemokine; thrombolytic; drug screening; arthritis; inflammation;
XX leukaemia.
XX
XX Homo sapiens.
XX
XX WO20015312-A1.
XX
XX 26-JUL-2001.
XX
XX 26-DEC-2000; 2000WO-US34263.
XX
XX 21-JAN-2000; 2000US-0488725.
XX 25-APR-2000; 2000US-0552317.
XX 09-JUL-2000; 2000US-0598042.
XX 19-JUL-2000; 2000US-0620312.
XX 03-AUG-2000; 2000US-0653450.
XX 14-SEP-2000; 2000US-0662191.
XX 19-OCT-2000; 2000US-0693036.
XX 29-NOV-2000; 2000US-0727344.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX Wang Z, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
XX Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI: 2001-442253/47.
XX N-PSDB: AAI58055.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders
XX such as central nervous system injuries -
XX
XX Example 3; SEQ ID NO 2044; 10078pp; English.
XX
XX The invention relates to human nucleic acids (AA157798-AA161369) and
XX the encoded polypeptides (AAM38642-AA42213) with neotropic.
XX CC immunosuppressant and cytostatic activity. The polynucleotides are useful
XX CC in gene therapy. A composition containing a polypeptide or polynucleotide
XX CC of the invention may be used to treat diseases of the peripheral nervous
XX CC system, such as peripheral nervous injuries, peripheral neuropathy and
XX CC localised neuropathies and central nervous system diseases, such as
XX CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX CC utilisation of the activities such as: Immune system suppression,
XX CC activin/inhibin activity, chemotactic/chemokine activity, haemostatic
XX CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX CC assays for receptor activity, arthritis and inflammation, leukemias and
XX CC C.N.S disorders.
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification.
XX
XX Sequence 227 AA;
```

Query Match 99.6%; Score 1156; DB 22; Length 227;
 Best Local Similarity 99.1%; Pred. No. 2.7e-111;
 Matches 225; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGASARLRRAVIMGAPSGKGVSSRITTHFELKHLSSGDLRDMLRGTETIGVLAKAFI 60
 |||
 DB 1 MGASARLRRAVIMGAPSGKGVSSRITTHFELKHLSSGDLRDMLRGTETIGVLAKAFI 60
 |||
 QY 61 DOGKLIPDDVMTRLALHEKNTLOYSWLDGFPRTLPOAEALDRAYQIDTVINLVNPFV 120
 |||
 DB 61 DOGKLIPDDVMTRLALHEKNTLOYSWLDGFPRTLPOAEALDRAYQIDTVINLVNPFV 120
 |||
 QY 121 IKORLTARWIHPASGRVNIIEFNPKTVGIDDLTGEPILQREDDKPEYIKRLKAYEDOT 180
 |||
 DB 121 IKORLTARWIHPASGRVNIIEFNPKTVGIDDLTGEPILQREDDKPEYIKRLKAYEDOT 180
 |||
 QY 181 KXVLXYQKKGVLFTFSGTETNKIMPYVYAFLOTKVPORSQKASVTP 227
 |||
 DB 181 KXVLXYQKKGVLFTFSGTETNKIMPYVYAFLOTKVPORSQKASVTP 227
 |||

RESULT 4
 AAB92887
 ID AAB92887 standard; Protein; 227 AA.
 XX AAB92887;
 AC
 XX 26-JUN-2001 (first entry)
 DT
 XX Human protein sequence SEQ ID NO:11492.
 DE
 XX Human; primer: detection; diagnosis; antisense therapy; gene therapy.
 KW
 XX Homo sapiens.
 OS
 XX EP1074617-A2.
 PN
 XX 07-FEB-2001.
 PD
 XX 28-JUL-2000; 2000EP-0116126.
 PF
 XX 29-JUL-1999; 99JP-0248036.
 PR 27-AUG-1999; 99JP-0300253.
 PR 11-JAN-2000; 2000JP-0118776.
 PR 02-MAY-2000; 2000JP-0183767.
 PR 09-JUN-2000; 2000JP-0241899.
 XX
 XX (HELI-) HELIX RES INST.
 PA
 XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX WPI: 2001-318749/34.
 DR
 XX
 XX Primer sets for synthesizing polynucleotides, particularly the 5602
 PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length cDNAs -
 XX
 XX Claim 8; SEQ ID 11492; 2537bp + CD ROM; English.
 PS
 XX The present invention describes primer sets for synthesizing 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in

CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.

Sequence 227 AA:
 SQ
 Query Match 99.6%; Score 1156; DB 22; Length 227;
 Best Local Similarity 99.1%; Pred. No. 2.7e-111;
 Matches 225; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGASARLRRAVIMGAPSGKGVSSRITTHFELKHLSSGDLRDMLRGTETIGVLAKAFI 60
 |||
 DB 1 MGASARLRRAVIMGAPSGKGVSSRITTHFELKHLSSGDLRDMLRGTETIGVLAKAFI 60
 |||
 QY 61 DOGKLIPDDVMTRLALHEKNTLOYSWLDGFPRTLPOAEALDRAYQIDTVINLVNPFV 120
 |||
 DB 61 DOGKLIPDDVMTRLALHEKNTLOYSWLDGFPRTLPOAEALDRAYQIDTVINLVNPFV 120
 |||
 QY 121 IKORLTARWIHPASGRVNIIEFNPKTVGIDDLTGEPILQREDDKPEYIKRLKAYEDOT 180
 |||
 DB 121 IKORLTARWIHPASGRVNIIEFNPKTVGIDDLTGEPILQREDDKPEYIKRLKAYEDOT 180
 |||
 QY 181 KXVLXYQKKGVLFTFSGTETNKIMPYVYAFLOTKVPORSQKASVTP 227
 |||
 DB 181 KXVLXYQKKGVLFTFSGTETNKIMPYVYAFLOTKVPORSQKASVTP 227
 |||

RESULT 5
 AAB93066
 ID AAB93066 standard; Protein; 227 AA.
 XX AAB93066;
 AC
 XX 26-JUN-2001 (first entry)
 DT
 XX Human protein sequence SEQ ID NO:11883.
 DE
 XX Human; primer: detection; diagnosis; antisense therapy; gene therapy.
 KW
 XX Homo sapiens.
 OS
 XX EP1074617-A2.
 PN
 XX 07-FEB-2001.
 PD
 XX 28-JUL-2000; 2000EP-0116126.
 PF
 XX 29-JUL-1999; 99JP-0248036.
 PR 27-AUG-1999; 99JP-0300253.
 PR 11-JAN-2000; 2000JP-0118776.
 PR 02-MAY-2000; 2000JP-0183767.
 PR 09-JUN-2000; 2000JP-0241899.
 XX
 XX (HELI-) HELIX RES INST.
 PA
 XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX WPI: 2001-318749/34.
 DR
 XX
 XX Primer sets for synthesizing polynucleotides, particularly the 5602
 PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length cDNAs -
 XX
 XX Claim 8; SEQ ID 11883; 2537bp + CD ROM; English.
 PS

XX The present invention describes primer sets for synthesizing 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.

XX Sequence 227 AA:
SQ

Query Match 99.6%; Score 1156; DB 22; Length 227;
Best Local Similarity 99.1%; Pred. No. 2.7e-111;
Matches 225; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 MGASARLLRAVIMGAPSGSGKTGVSRRITTHFEKLHSSGDLRLDNLRGTEIGVLAKAFI 60
DB 1 MGASARLLRAVIMGAPSGSGKTGVSRRITTHFEKLHSSGDLRLDNLRGTEIGVLAKAFI 60
OY 61 DQGLIPDDVMTRALHEKLNLTQYSWLDGFPRTLPQAEALDRAYQIDTVINLVNPFVEY 120
DB 61 DQGLIPDDVMTRALHEKLNLTQYSWLDGFPRTLPQAEALDRAYQIDTVINLVNPFVEY 120
OY 121 IKORLTARMIHPASGRVYNIENFPKTVGIDLTGEPRLQREDDKRETYIKRLKAVEDOT 180
DB 121 IKORLTARMIHPASGRVYNIENFPKTVGIDLTGEPRLQREDDKRETYIKRLKAVEDOT 180
OY 181 KXVLYYOKKGVLETFSGTETNKIMPYVYAFLOTKVPQORSOKASVTP 227
DB 181 KXVLYYOKKGVLETFSGTETNKIMPYVYAFLOTKVPQORSOKASVTP 227

RESULT 6

AAB93487
ID AAB93487 standard; Protein: 227 AA.

XX AAB93487;

XX 26-JUN-2001 (first entry)

DE Human protein sequence SEQ ID NO.12786.

XX Human; primer: detection; diagnosis; antisense therapy; gene therapy.

XX Homo sapiens.

XX EP1074617-A2.

XX 07-FEB-2001.

XX 28-JUL-2000; 2000EP-0116126.

XX 29-JUL-1999; 99JP-0248036.

XX 27-AUG-1999; 99JP-0300253.

XX 11-JAN-2000; 2000JP-0118776.

XX 02-MAY-2000; 2000JP-0183767.

XX 09-JUN-2000; 2000JP-0241899.

PA (HELI-) HELIX RES INST.
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
DR WPI: 2001-318749/34.

PT Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -

PS Claim 8; SEQ ID 12786: 2537bp + CD ROM; English.

XX The present invention describes primer sets for synthesizing 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.

SQ Sequence 227 AA:

Query Match 99.6%; Score 1156; DB 22; Length 227;
Best Local Similarity 99.1%; Pred. No. 2.7e-111;
Matches 225; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 MGASARLLRAVIMGAPSGSGKTGVSRRITTHFEKLHSSGDLRLDNLRGTEIGVLAKAFI 60
DB 1 MGASARLLRAVIMGAPSGSGKTGVSRRITTHFEKLHSSGDLRLDNLRGTEIGVLAKAFI 60
OY 61 DQGLIPDDVMTRALHEKLNLTQYSWLDGFPRTLPQAEALDRAYQIDTVINLVNPFVEY 120
DB 61 DQGLIPDDVMTRALHEKLNLTQYSWLDGFPRTLPQAEALDRAYQIDTVINLVNPFVEY 120
OY 121 IKORLTARMIHPASGRVYNIENFPKTVGIDLTGEPRLQREDDKRETYIKRLKAVEDOT 180
DB 121 IKORLTARMIHPASGRVYNIENFPKTVGIDLTGEPRLQREDDKRETYIKRLKAVEDOT 180
OY 181 KXVLYYOKKGVLETFSGTETNKIMPYVYAFLOTKVPQORSOKASVTP 227
DB 181 KXVLYYOKKGVLETFSGTETNKIMPYVYAFLOTKVPQORSOKASVTP 227

RESULT 7

AAB85885
ID AAB85885 standard; Protein: 227 AA.

XX AAB85885;

XX 30-NOV-2001 (first entry)

DE Human adenylate kinase 3 (AK3)-like protein.

XX Adenylate kinase 3-like protein; AK3-like protein; AK3; cell morphology;

XX MELAS; central nervous system disorder; epilepsy; skeletal muscle;

KW muscle disease; electron transfer disorder; Leber disease; human;

KW diabetes mellitus; Peason disease; Parkinson's disease.
XX Homo sapiens.
OS
XX WO200109346-A1.
XX
XX 08-FEB-2001.
XX
XX 28-JUL-2000; 2000WO-JP05066.
XX
XX 29-JUL-1999; 99JP-0248036.
XX 27-AUG-1999; 99JP-0300253.
XX 18-OCT-1999; 99US-0159590.
XX 11-JAN-2000; 2000JP-0118776.
XX 17-FEB-2000; 2000US-0183322.
XX
XX (HELI-) HELIX RES INST.
XX
XX Ota T, Isogai T, Hayashi K, Saito K, Yamamoto J, Ishii S;
PI Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Ihara S, Nakae H;
PI Nishikawa T, Kimura K;
XX
XX MPI: 2001-564737/63.
XX N-PSDB: AAA47197.
XX
XX
XX New gene encoding an adenylyate kinase 3-like protein, and the protein
PT and antibodies to it, useful for diagnosis of brain disease e.g.
PT epilepsy, muscle disease, genetic disorder, diabetes -
XX
XX
XX Claim 1: Page 34-35; 41pp; Japanese.
XX
XX The invention relates to a cDNA (clone C-NT2RP2000329) encoding a novel
CC adenylyate kinase 3 (AK3)-like protein. C-NT2RP2000329 has functions of
CC converting extracellular signals into intracellular signals and changing
CC cell morphology. The AK3-like protein, polynucleotides and antibodies are
CC useful in the investigation of diseases such as MELAS (cerebral accident
CC condition with hyperlactacidemia), central nervous system disorder,
CC epilepsy, skeletal muscle conditions, muscle disease, electron transfer
CC disorders, Leber disease, diabetes mellitus, Peason disease, Parkinson's
CC disease, metabolism disorders. They are useful for developing diagnostics
CC and treatment agents. The present sequence represents the human AK3-like
CC protein of the invention.
XX
XX
XX Sequence 227 AA:
SQ
Query Match 99.6%; Score 1156; DB 22; Length 227;
Best Local Similarity 99.1%; Pred. No. 2,7e-111;
Matches 225; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MGASARLLRAVIMGAPSGSGKTVSSRITTHFELKHLSSGDLRLDMLRGTEIGVLAKAFI 60
DB 1 MGASARLLRAVIMGAPSGSGKTVSSRITTHFELKHLSSGDLRLDMLRGTEIGVLAKAFI 60
QY 61 DOGKLIIPDVWTRALHLEKLNITQYSWLLDGFPRRLPOAEALDRAKYQIDTYINLWVPEV 120
DB 61 DOGKLIIPDVWTRALHLEKLNITQYSWLLDGFPRRLPOAEALDRAKYQIDTYINLWVPEV 120
QY 121 IKORLTAMWIPASGRVNIENFPKTYGIDDLTGEPIQREDDPEYIKRLKAYEDOT 180
DB 121 IKORLTAMWIPASGRVNIENFPKTYGIDDLTGEPIQREDDPEYIKRLKAYEDOT 180
QY 181 KXVLXYOKKGVLETFSGTETNKKIMPVYVAFLOTRKVPORSOKASYTP 227
DB 181 KPVLEYOKKGVLETFSGTETNKKIMPVYVAFLOTRKVPORSOKASYTP 227
RESULT 8
ABBI2326
ID ABBI2326 standard; peptide: 239 AA.
XX
XX AC ABBI2326;
XX
XX 11-JAN-2002 (first entry)

XX
DE Human secreted protein homologue, SEQ ID NO:2696.
KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytosolic; osteopathic; vasotropic; cardiant; vitucide; antibacterial;
KW antifungal; vulnerrary; antulcer.
XX
XX Homo sapiens.
OS
XX WO200157188-A2.
XX
XX 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US03800.
XX
XX 03-FEB-2000; 2000US-0496914.
XX 27-APR-2000; 2000US-0560875.
XX
XX (HXSE-) HXSEQ INC.
XX
XX Tang YF, Liu C, Drmanac RT;
PI MPI: 2001-457740/49.
XX N-PSDB: ABA09570.
XX
XX Human proteins and DNA encoding sequences useful for preventing,
PT treating or ameliorating a medical condition in a mammalian subject
PT e.g. arthritis and cancer -
XX
XX
XX Claim 20; Page 333; 1963pp; English.
XX
XX Sequences ABBI0981-ABBI2330 represent 1350 novel human polypeptides, and
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC invention also relates to vectors and recombinant host cells comprising a
CC nucleotide of the invention, methods of producing the novel polypeptides,
CC antibodies against the polypeptides, methods of detecting the nucleotides
CC or polypeptides in a sample, and methods of identifying compounds which
CC bind to polypeptides of the invention. Although novel, many of the
CC polypeptides of the invention have homology to known proteins, thereby
CC giving an insight into their probable biological activities, and hence
CC potential therapeutic applications. The polypeptides of the invention may
CC have various activities, including cytokine, cell proliferation or cell
CC differentiation activities, stem cell growth factor activity;
CC haematopoiesis regulatory activity; tissue growth activity;
CC immunomodulatory activity; activin- or inhibin-related activities;
CC chemoatctic or chemokinetic activities; haemostatic, thrombotic or
CC thrombolytic activities; receptor or ligand activities; or may be
CC involved in oncogenesis, cancer cell proliferation or metastasis.
CC Depending on their biological activities, polypeptides and nucleotides of
CC the invention are useful for preventing, treating or ameliorating medical
CC conditions, e.g., by protein or gene therapy. Such conditions include
CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC proliferative retinopathy, atherosclerosis, coronary heart disease,
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC vascular growth. Polypeptides involved with tissue regeneration and
CC repair (or nucleic acids encoding them) may be used to promote wound
CC healing (e.g., of burns, incisions and ulcers), while those with
CC immunomodulatory activities may be used in the treatment of viral,
CC bacterial and fungal infections in addition to immune disorders.
CC Polypeptides with growth factor activity may be used in cell cultures to
CC promote cell growth. For example, such polypeptides may be used to
CC manipulate stem cells in culture to give rise to neuroepithelial cells

CC that can be used to augment or replace cells damaged by illness,
CC autoimmune disease or accidental damage. The polypeptides and nucleotides
CC may also be used in the diagnosis of the above conditions, and in drug
CC screening techniques. The present sequence represents a novel human
CC polypeptide of the invention.

XX SQ Sequence 239 AA:

Query Match 99.6%; Score 1156; DB 22; Length 239;
Best Local Similarity 99.1%; Pred. No. 2,9e-111;
Matches 225; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGASARLLRAVIMGAPSGKGVSSRITTHFEKHLSSGDLRDNMRLRGTEIGVLAFAFI 60
DB 13 MGASARLLRAVIMGAPSGKGVSSRITTHFEKHLSSGDLRDNMRLRGTEIGVLAFAFI 72
QY 61 DQGLIPDDVMTRLALHELKNTQYSWLDGFPRTLPOAEALDRAVOIDVINLNVPFEV 120
DB 73 DQGLIPDDVMTRLALHELKNTQYSWLDGFPRTLPOAEALDRAVOIDVINLNVPFEV 132
QY 121 IKQRLTARWTHIPASGRVYNIEFNPPTKTVGIDLTGEPILIOREDDKPETVIKRLKAYEDQT 180
DB 133 IKQRLTARWTHIPASGRVYNIEFNPPTKTVGIDLTGEPILIOREDDKPETVIKRLKAYEDQT 192
QY 181 KXVLXYQKKGVLTFESGTEFNKIWPYVAFLOTQKVPORSOKASVTP 227
DB 193 KXVLXYQKKGVLTFESGTEFNKIWPYVAFLOTQKVPORSOKASVTP 239

RESULT 9
AAM40685

ID AAM40685 standard; Protein: 239 AA.

XX AC AAM40685;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 5616.

XX KW Human; noctropic; immunosuppressant; cytostatic; gene therapy; cancer;
XX KW peripheral nervous system; neuropathy; central nervous system; CNS;
XX KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
XX KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
XX KW leukaemia.

XX OS Homo sapiens.

XX PN WO200153312-A1.

XX PD 26-JUL-2001.

XX PF 26-DEC-2000; 200OWO-US34263.

XX PR 21-JAN-2000; 2000US-0488725.
XX PR 25-APR-2000; 2000US-0552317.
XX PR 09-JUL-2000; 2000US-0598042.
XX PR 19-JUL-2000; 2000US-0620312.
XX PR 03-AUG-2000; 2000US-0653450.
XX PR 14-SEP-2000; 2000US-0662191.
XX PR 19-OCT-2000; 2000US-0693036.
XX PR 29-NOV-2000; 2000US-0727344.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX PI Wang J, Wang Z, Weinman T, Xu C, Xue AJ, Yang Y, Zhang J;
XX PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;

XX DR WPI: 2001-442253/47.

XX DR N-PSDB; AA159841.

XX PT Novel nucleic acids and polypeptides, useful for treating disorders

PT such as central nervous system injuries -
XX
XX Example 2; SEQ ID NO 5616; 10078bp; English.

CC The invention relates to human nucleic acids (AA157798-AA161369) and
CC the encoded polypeptides (AAM38642-AAM42213) with noctropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.

XX SQ Sequence 239 AA:

Query Match 99.6%; Score 1156; DB 22; Length 239;
Best Local Similarity 99.1%; Pred. No. 2,9e-111;
Matches 225; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGASARLLRAVIMGAPSGKGVSSRITTHFEKHLSSGDLRDNMRLRGTEIGVLAFAFI 60
DB 13 MGASARLLRAVIMGAPSGKGVSSRITTHFEKHLSSGDLRDNMRLRGTEIGVLAFAFI 72
QY 61 DQGLIPDDVMTRLALHELKNTQYSWLDGFPRTLPOAEALDRAVOIDVINLNVPFEV 120
DB 73 DQGLIPDDVMTRLALHELKNTQYSWLDGFPRTLPOAEALDRAVOIDVINLNVPFEV 132
QY 121 IKQRLTARWTHIPASGRVYNIEFNPPTKTVGIDLTGEPILIOREDDKPETVIKRLKAYEDQT 180
DB 133 IKQRLTARWTHIPASGRVYNIEFNPPTKTVGIDLTGEPILIOREDDKPETVIKRLKAYEDQT 192
QY 181 KXVLXYQKKGVLTFESGTEFNKIWPYVAFLOTQKVPORSOKASVTP 227
DB 193 KXVLXYQKKGVLTFESGTEFNKIWPYVAFLOTQKVPORSOKASVTP 239

RESULT 10

AAG73865

ID AAG73865 standard; Protein: 256 AA.

XX AC AAG73865;

XX DT 03-SEP-2001 (first entry)

XX DE Human colon cancer antigen protein SEQ ID NO:4629.

XX KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
XX KW colorectal carcinoma.

XX OS Homo sapiens.

XX PN WO200122920-A2.

XX PD 05-APR-2001.

XX PF 28-SEP-2000; 200OWO-US26524.

XX PR 29-SEP-1999; 99US-0157137.
XX PR 03-NOV-1999; 99US-0163280.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ruben SM, Barash SC, Birse CE, Rosen CA;

XX DR WPI: 2001-235357/24.

DR N-PSDB; AAH3296.
XX
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT useful for preventing, diagnosing and/or treating colorectal cancers -
XX
XX
PS Claim 11: Page 6430-6431; 9803pp; English.
XX
CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where
CC the proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene
CC therapy and vaccine production. N and P may be used in the prevention,
CC diagnosis and treatment of diseases associated with inappropriate P
CC expression. For example, N and P may be used to treat disorders
CC associated with decreased expression by rectifying mutations or deletions
CC in a patient's genome that affect the activity of P by expressing
CC inactive proteins or to supplement the patient's own production of P.
CC Additionally, N may be used to produce the colon cancer-associated Ps,
CC by inserting the nucleic acids into a host cell and culturing the cell
CC to express the proteins. N and P can be used in the prevention, diagnosis
CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
CC and AAG77789 represent sequences used in the exemplification of the
CC present invention.
CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
CC missing at time of publication, meaning no sequences are present for
CC SEQ ID NO:1027 to 1052, 7921 and 7922.
XX
SQ Sequence 256 AA:
Query Match 99.6%; Score 1156; DB 22; Length 256;
Best Local Similarity 99.1%; Pred. No. 3.2e-111;
Matches 225; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MGASARLRAVIMGAPGSGKGVSSRTTHFEELKHLSSGDLRDNNLRGTEIGVLAKAFI 60
DB 30 MGASARLRAVIMGAPGSGKGVSSRTTHFEELKHLSSGDLRDNNLRGTEIGVLAKAFI 89
QY 61 DQGLIPDDVMTRLALHELKNTQYSMLDGFPRTLPOAEALDRAYQIDTVINLVNPFVEY 120
DB 90 DQGLIPDDVMTRLALHELKNTQYSMLDGFPRTLPOAEALDRAYQIDTVINLVNPFVEY 149
QY 121 IKORLTARMIHPASGRVNIIEFNPKTVGIDDLTGEPILQREDDKPEYIKRLKAYEDQT 180
DB 150 IKORLTARMIHPASGRVNIIEFNPKTVGIDDLTGEPILQREDDKPEYIKRLKAYEDQT 209
QY 181 KXVLYYQKKGVLETFSGTETNKIMPYVAFLOTKVPRQSRKASVTP 227
DB 210 KXVLYYQKKGVLETFSGTETNKIMPYVAFLOTKVPRQSRKASVTP 256
RESULT 11
AAB12440
ID AAB12440 standard; Protein; 227 AA.
XX
AC AAB12440;
XX
DT 20-OCT-2000 (first entry)
XX
DE Human mitochondrial GTP:AMP phosphotransferase SEQ ID NO:4.
XX
KW Human; mitochondrial GTP:AMP phosphotransferase; GTP3P; ribotide.
XX
OS Homo sapiens.
XX
PN CN1249340-A.
XX
PD 05-APR-2000.
XX
XX 28-SEP-1998; 98CN-0119439.
XX
PR 28-SEP-1998; 98CN-0119439.
XX
PA (XINH-) XINHUANGPU FUDAN GENE ENG CO LTD SHANGHA.

XX
PI Yu L, Zhao Y, Bi A;
XX
XX WPI; 2000-400718/35.
DR N-PSDB; AAA60582.
XX
PT Preparation of human mitochondrial matrix GTP : AMP phosphotransferase,
PT its encode sequence -
XX
XX Claim 4: Page 14-15; 20pp; Chinese.
XX
CC The present invention describes a new ribotide sequence of human gene,
CC that is, the cDNA sequence of human mitochondrial matrix GTP:AMP
CC phosphotransferase (GTP3P) and the encoded polypeptide. The present
CC sequence represents human GTP3P.
XX
SQ Sequence 227 AA:
Query Match 97.3%; Score 1130; DB 21; Length 227;
Best Local Similarity 97.4%; Pred. No. 1.3e-108;
Matches 221; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 1 MGASARLRAVIMGAPGSGKGVSSRTTHFEELKHLSSGDLRDNNLRGTEIGVLAKAFI 60
DB 1 MGASARLRAVIMGAPGSGKGVSSRTTHFEELKHLSSGDLRDNNLRGTEIGVLAKAFI 60
QY 61 DQGLIPDDVMTRLALHELKNTQYSMLDGFPRTLPOAEALDRAYQIDTVINLVNPFVEY 120
DB 61 DQGLIPDDVMTRLALHELKNTQYSMLDGFPRTLPOAEALDRAYQIDTVINLVNPFVEY 120
QY 121 IKORLTARMIHPASGRVNIIEFNPKTVGIDDLTGEPILQREDDKPEYIKRLKAYEDQT 180
DB 121 IKORLTARMIHPASGRVNIIEFNPKTVGIDDLTGEPILQREDDKPEYIKRLKAYEDQT 180
QY 181 KXVLYYQKKGVLETFSGTETNKIMPYVAFLOTKVPRQSRKASVTP 227
DB 181 KXVLYYQKKGVLETFSGTETNKIMPYVAFLOTKVPRQSRKASVTP 227
RESULT 12
AAB12441
ID AAB12441 standard; Protein; 227 AA.
XX
AC AAB12441;
XX
DT 20-OCT-2000 (first entry)
XX
DE AK3 protein sequence.
XX
KW Human; mitochondrial GTP:AMP phosphotransferase; GTP3P; ribotide.
XX
OS Unidentified.
XX
PN CN1249340-A.
XX
PD 05-APR-2000.
XX
XX 28-SEP-1998; 98CN-0119439.
XX
PR 28-SEP-1998; 98CN-0119439.
XX
PA (XINH-) XINHUANGPU FUDAN GENE ENG CO LTD SHANGHA.
XX
PI Yu L, Zhao Y, Bi A;
XX
XX WPI; 2000-400718/35.
DR N-PSDB; AAA60585.
XX
PT Preparation of human mitochondrial matrix GTP : AMP phosphotransferase,
PT its encode sequence -
XX
XX Example 2; Fig 2; 20pp; Chinese.

CC The present invention describes a new ribotide sequence of human gene,
 CC that is, the cDNA sequence of human mitochondrial matrix GTP:AMP
 CC phosphotransferase (GTP3P) and the encoded polypeptide. The present
 CC sequence represents the AK3 protein sequence which is used in
 CC comparison with human GTP3P in the present invention.

CC Sequence 227 AA:

Query Match 94.0%; Score 1091; DB 21; Length 227;

Best Local Similarity 91.6%; Pred. No. 1.5e-104;

Matches 208; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 MGASABLLRAVINGAPSGKGVSSRITTFHELKHLSSGDLRDMLRGTEIGVLAKAFI 60

DB 1 MGASABLLRAVINGAPSGKGVSSRITTFHELKHLSSGDLRDMLRGTEIGVLAKAFI 60

QY 61 DQGLIPDDVMTRLALHELKNTQYSMLDGFPRTLPOAEALDRAYQIDVTINLNPFEV 120

DB 61 DQGLIPDDVMTRLALHELKNTQYSMLDGFPRTLPOAEALDRAYQIDVTINLNPFEV 120

QY 121 IKORLARARITHPASGRVYNIENPPTKVGIDLTGEPLQREDDKPEYIKRLKAYEDQT 180

DB 121 IKORLARARITHPASGRVYNIENPPTKVGIDLTGEPLQREDDKPEYIKRLKAYEAO 180

QY 181 KXVLYTOKKGVLEFSGTETNKIMPYVYAFLOTQVPORSQKASVMP 227

DB 181 EPVLEYRKKGVLFTSGTETNKIMPHYVAFLOTQLPQSQETSVP 227

RESULT 13

AAB53619

ID AAB53619 standard; Protein; 214 AA.

XX AAB53619;

DT 09-MAR-2001 (first entry)

DE Human colon cancer antigen protein sequence SEQ ID NO:1159.

XX Human; colon cancer; colon cancer antigen; diagnosis; detection;

KW Identification; cytosolic; cardioactive; neuroprotective; vulnary;

KW Immunomodulatory; muscular; gynaecological; gastrointestinal;

KW nephrotropic; antiinfective; antibacterial; gene therapy; wound;

KW neural disorder; immune system disorder; muscular disorder;

KW reproductive disorder; gastrointestinal disorder; renal disorder;

KW infectious disease; cardiovascular disorder.

XX Homo sapiens.

OS (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM;

XX WPI: 2000-587534/55.

DR N-PSDB: AAC98376.

XX Colon cancer associated gene sequences, referred to as colon cancer

PS Claim 11; Page 1741-1742; 2104pp; English.

CC AAC97991 to AAC98763 encode the human colon cancer associated proteins,

CC called human colon cancer antigens, given in AAB53334 to AAB54006. The

CC human colon cancer antigens can have cytosolic, cardioactive, muscular;

CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal,
 CC vulnerary, nephrotropic, antiinfective and antibacterial activities, and
 CC can be used in gene therapy. The colon cancer antigen polynucleotides,
 CC proteins and antibodies to the proteins are useful for the prevention,
 CC treatment and diagnosis of colon disorders, such as colon cancer. The
 CC polynucleotides may be used in diagnostics and research, such as for
 CC chromosome identification, and as hybridisation probes. The proteins
 CC may also be used to prevent diseases such as neural disorders, immune
 CC system disorders, muscular disorders, reproductive disorders,
 CC gastrointestinal disorders, wounds, renal disorders, infectious
 CC diseases, and cardiovascular disorders. AAC98764 to AAC98772 and
 CC AAB54007 represent sequences used in the exemplification of the present
 CC invention.

CC Sequence 214 AA:

Query Match 90.3%; Score 1048; DB 21; Length 214;

Best Local Similarity 95.3%; Pred. No. 3.8e-100;

Matches 203; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 10 AVIMGAPSGKGVSSRITTFHELKHLSSGDLRDMLRGTEIGVLAKAFIDQGLIPDD 69

DB 1 AVIMGAPSGKGVSSRITTFHELKHLSSGDLRDMLRGTEIGVLAKAFIDQGLIPDD 60

QY 70 VMTRLALHELKNTQYSMLDGFPRTLPOAEALDRAYQIDVTINLNPFEVIRKRLTARW 129

DB 61 VMTRLALHELKNTQYSMLDGFPRTLPOAEALDRAYQIDVTINLNPFEVIRKRLTARW 120

QY 130 IHPASGRVYNIENPPTKVGIDLTGEPLQREDDKPEYIKRLKAYEDQTKXVLYYOK 189

DB 121 IHPASGRVYNIENPPTKVGIDLTGEPLQREDDKPEYIKRLKAYEDQTKVLEYOK 180

QY 190 KGVLEFSGTETNKIMPYVYAFLOTQVPORSQK 222

DB 181 KGVLEFSGTETNKIMPYVYAFLOTQVPORSQK 213

RESULT 14

AAB51778

ID AAB51778 standard; Protein; 224 AA.

XX AAB51778;

DT 18-DEC-2001 (first entry)

DE Human kinase (PKIN)-12 protein.

XX Human kinase; PKIN; gene therapy; adenocarcinoma; immune disorder; gout;

KW cancer; allergy; sarcoma; leukaemia; acquired immune deficiency syndrome;

KW AIDS; Addison's disease; microbial infection; inflammation; osteoporosis;

KW atherosclerosis; cardiovascular disease; myocardial infarction; anaemia;

KW myasthenia gravis; cirrhosis; cataract; growth and development disorder;

KW seizure disorder; pulmonary embolism; Gaucher's disease; lipid disorder;

KW lipid storage disease; Pick's disease; Ray-Sachs disease; renal disease;

KW obesity; restorative therapy; immunomodulatory; vaccine; cardiovascular;

KW antimicrobial; cytosolic; antiinflammatory; asthma.

XX Homo sapiens.

OS

XX Key

FT Location/Qualifiers

FT 1..126

FT Region

FT /note="Adenylate kinase"

FT 8..23

FT Region

FT /note="Shikimate kinase family"

FT 9..25

FT Region

FT /note="Adenylate kinase"

FT 10..190

FT Region

FT /note="Adenylate kinase"

FT 33..76

FT Region

FT /note="Adenylate kinase"

FT 80..94

FT Region

FT /note="Adenylate kinase"

FT 85..96

FT Domain

FT /note="Adenylate kinase motif"
ET 107..124
FT /note="Shikimate kinase family"
ET Region 132..162
ET /note="Adenylate kinase"
XX
XX WO200181555-A2.
XX
XX 01-NOV-2001.
XX
XX 20-APR-2001; 2001WO-US12992.
XX
XX 20-APR-2000; 2000US-199021P.
PR 28-APR-2000; 2000US-200226P.
PR 05-MAY-2000; 2000US-200239P.
PR 11-MAY-2000; 2000US-203505P.
PR 18-MAY-2000; 2000US-205564P.
PR 26-MAY-2000; 2000US-207339P.
PR 01-JUN-2000; 2000US-208795P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Yue H, Gandhi AR, Tribouley CM, Kearney L, Griffin JA, Nguyen DB;
PI Bandman O, Lu DM, Lal P, Burford N, Khan FA, Walla NK, Yao MG;
PI Patterson C, Burill JD, Marcus GA, Ziegler KA, Rectipon SA, Lu Y;
PI Policky JB, Thornton M, Tang YT, Hafalia A, Elliott VS, Baughn MR;
PI Walsh RT, Ramkumar J, Borowsky ML, Au-young J, Hillman JL;
PI Gururajan R;
XX
XX WPI: 2001-611740/70.
DR N-PSDB; AAD18627.
XX
XX Human kinases and nucleic acids, useful for preventing diagnosing and
PT treating cancers, inflammation and immune disorders -
XX
XX Claim 1: Page 138-139; 166pp; English.
XX
XX The present invention relates to human kinases (PKIN) and the nucleic
CC acids encoding them. PKIN is used as vaccine and in gene therapy. PKIN is
CC used in the prevention, diagnosis and treatment of diseases cancers,
CC adenocarcinoma, leukemia, sarcoma, immune disorder, Addison's disease,
CC acquired immune deficiency syndrome (AIDS), anemia, asthma, allergies,
CC gout, microbial infections, cardiovascular disease and/or inflammation,
CC myasthenia gravis, atherosclerosis, cirrhosis, osteoporosis, myocardial
CC infarction, cataract, growth and development disorder, seizure disorder,
CC pulmonary embolism, Gaucher's disease, lipid disorder, lipid storage
CC disease, Pick's disease, Tay-Sachs disease, renal disease and obesity.
CC PKIN may be used to treat disorders associated with decreased PKIN
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of PKIN by expressing inactive proteins or to
CC supplement the patients own production of PKIN. PKIN nucleic acids may be
CC used to produce the PKIN polypeptide, by inserting the nucleic acids into
CC a host cell and culturing the cell to express the protein. PKIN nucleic
CC acid and its complementary sequences may also be used as DNA probes in
CC diagnostic assays to detect and quantitate the presence of similar
CC nucleic acid sequences in samples and therefore which patients may be
CC in need of restorative therapy. The present sequence is human PKIN-12
CC protein.
XX
XX Sequence 224 AA;
XX
XX Query Match 56.4%; Score 655; DB 22; Length 224;
XX Best Local Similarity 56.3%; Pred. No. 1.9e-59;
XX Matches 125; Conservative 38; Mismatches 57; Indels 2; Gaps 2;

Qy 4 SARLRAYIMGAPSGKGVSSRITTHFEIKHLSGDLRLDMMLAGTEGVAKAFIOG 63
Db 2 ASKLRAVILPGSGKGVCCORIAQNGLOLSSGHFLREIKASTGEENAKOYIKS 61
Qy 64 KLIPDVMVRLALHKLNLTOYSMLLDGFPRTLPOAEALDRAYQIDVTYNLWPEVIRK 123
Db 62 LLVPDHVITRLMSELENRROGHMLLDGFPRTLGOAEALDKCEVDIVISLNIPRETIKD 121

Qy 124 RLTAHWHPASGRVYNIENPPKTVGIDDLTCEPLIQREDDKPEVYIKRLAYEDQTKXV 183
Db 122 RLSRRWHPSPGRVYLDENPPHVGIDVTEGPELVQGEDDKPEVAARQYKDVAKVY 181
Qy 184 LXYQKKGL-ETFGSTERNKIMPYVY-AFLQTKVPQRQKA 223
Db 182 IELYKSRGVLAHQFERNRRRTKIMPYVYTTFLNKTTPQSKEA 223
XX
XX RESULT 15
XX ABG23968
XX ID ABG23968 standard; Protein; 335 AA.
XX
XX ABG23968;
XX AC
XX 18-FEB-2002 (first entry)
XX DT
XX DE Novel human diagnostic protein #23959.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX Homo sapiens.
XX OS
XX WO200175067-A2.
XX PN
XX 11-OCT-2001.
XX PD
XX 30-MAR-2001; 2001WO-US08631.
XX PF
XX 31-MAR-2000; 2000US-0540217.
XX PR 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Dyrnaac RT, Liu C, Tang YT;
XX PI
XX WPI: 2001-639362/73.
DR N-PSDB; AAS86155.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
XX Claim 20: SEQ ID NO 54327; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 335 AA;
XX
XX Query Match 55.0%; Score 639; DB 22; Length 335;
XX Best Local Similarity 54.9%; Pred. No. 1.5e-57;

	Matches	123, Conservative	34, Mismatches	65, Indels	2, Gaps	2,
Qy	4	SARLLRAVINGAPSGGKGT-VSSRTITTHPELKHSGLDRDNLNRGIEIGYLAQ-AFLFD	61			
Db	80	ASKLLRAVITLCPGGKCAPVCAQRJAQNFGIOLHSSGFLRENIKASTVEGMAQVYRE	139			
Qy	62	QGLKLIPDDVMRLALHEKLNLTQYSMLNDGFPRTLPOAEALDRAVOIPVILANYPFEVI	121			
Db	140	KVELPDPVHVIITRLMSELENRRGQIMLLDGFPRITGQAEALDDICEVDLVLTINLSFETL	199			
Qy	122	KQRLTARMIHPASGVRVNIIEENPRTKVIDDITGEPILQIREDDEKPEYIKRLKAYEDQTK	181			
Db	200	KDGLNRRMIHPSPGSRVYMLDFNPPRHVHGIDVTGEPILVQOEDDKPEAAVARLRQYKDVAK	259			
Qy	182	XVLXXYQKKGLTEFSGTETNKIMPYVVAFLDTQKPSQKASV	225			
Db	260	PVIEILKSRGVLPQPSGTETNKIMPYVTLTSSNKLITTPIOSKESI	303			

Search completed: March 19, 2003, 16:03:22
Job time : 1049 secs

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GenCore version 5.1.4.p5_4578
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OM nucleic - nucleic search, using sw model

Run on: March 18, 2003, 19:59:24 ; Search time 31295 Seconds

(without alignments)
794.178 Million cell updates/sec

Title: US-10-006-190-2

Perfect score: 854
Sequence: 1 GCCANGCCCAAGCCCTGCT.....TGAATATATATTACTTTTA 854

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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GenEmbl: *
1: gb_ba: *
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5: gb_ov: *
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7: gb_ph: *
8: gb_pl: *
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10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
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21: em_or: *
22: em_ov: *
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24: em_ph: *
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27: em_sts: *
28: em_un: *
29: em_vl: *
30: em_htg_hum: *
31: em_htg_inv: *
32: em_htg_other: *
33: em_htg_mus: *
34: em_htg_pln: *
35: em_htg_rtd: *
36: em_htg_mam: *
37: em_htg_vrt: *
38: em_sy: *
39: em_htgo_hum: *
40: em_htgo_mus: *
41: em_htgo_other: *

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	851	99.6	854	6	AR027227	AR027227 Sequence
2	851	99.6	854	6	AR094188	AR094188 Sequence
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4	835.2	97.8	1701	9	AK001951	AK001951 Homo sapi
5	835.2	97.8	2642	9	AK001553	AK001553 Homo sapi
6	816	95.6	2394	6	BD012403	BD012403 Novel gen
7	816	95.6	2394	6	AK027534	AK027534 Homo sapi
8	816	95.6	2394	23	BD005083	BD005083 Novel gen
9	667.6	78.2	684	9	AB021870	AB021870 Homo sapi
10	653	76.5	1539	9	AF183419	AF183419 Homo sapi
11	653	76.5	3008	9	AK098205	AK098205 Homo sapi
12	613.6	71.9	3631	4	BOVPKIMP	M25757 Bovine mito
13	573.6	67.2	725	4	AF417508	AF417508 Oryctolab
14	573.4	67.1	1850	10	BC016432	BC016432 Mus muscu
15	573.4	67.1	1860	10	BC019174	BC019174 Mus muscu
16	573.4	67.1	2776	10	BC024871	BC024871 Mus muscu
17	572.4	67.0	77496	2	AC116062	AC116062 Rattus no
18	559.2	65.5	1061	10	RATKINASE3	D13062 Rat mRNA fo
19	542	63.5	973	10	AB020203	AB020203 Mus muscu
20	520.4	60.9	142080	2	AC069260	AC069260 Homo sapi
21	520.4	60.9	190253	2	AC067779	AC067779 Homo sapi
22	520.4	60.9	201821	2	AC129105	AC129105 Homo sapi
23	520.4	60.9	339569	2	AC107306	AC107306 Homo sapi
24	518.8	60.7	148643	2	AC011871	AC011871 Homo sapi
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26	518.8	60.7	183203	2	AC078930	AC078930 Homo sapi
27	518.8	60.7	190723	2	AC069262	AC069262 Homo sapi
28	465.2	54.5	153792	2	AC094097	AC094097 Homo sapi
29	465.2	54.5	197973	2	AL365203	AL365203 Homo sapi
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31	463.6	54.3	210378	2	AL590967	AL590967 Homo sapi
32	417	48.8	176257	9	AC006039	AC006039 Homo sapi
33	381.8	44.7	171381	9	AL162730	AL162730 Human DNA
34	337.8	39.6	209669	2	AC091949	AC091949 Homo sapi
35	337.8	39.6	214928	2	AC091981	AC091981 Homo sapi
36	332.2	38.9	208660	2	AC020577	AC020577 Homo sapi
37	332.2	38.9	214928	2	AC091981	AC091981 Homo sapi
38	301.2	35.3	133475	9	AC006254	AC006254 Homo sapi
39	299.6	35.1	174613	2	AC012522	AC012522 Homo sapi
40	258.4	30.3	162959	2	AC019255	AC019255 Homo sapi
41	258.4	30.3	168292	2	AC068774	AC068774 Homo sapi
42	258.4	30.3	210544	2	AC023157	AC023157 Homo sapi
43	258.2	30.2	2026	9	HSNA3PS	X60674 Human AK3 p
44	255.2	29.9	69631	2	AC126386	AC126386 Homo sapi
45	255.2	29.9	93102	2	AC126355	AC126355 Homo sapi

ALIGNMENTS

RESULT 1
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DEFINITION Sequence 2 from patent US 5856160.
ACCESSION AR027227
VERSION AR027227.1 GI:5938067
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 854)
AUTHORS Hillman,J.L. and Shah,P.
TITLE Mitochondrial adenylylate kinase
JOURNAL Patent: US 5856160-A 2 05-JAN-1999;
FEATURES Location/Qualifiers

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/organism="unknown"
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Query Match 99.6%; Score 851; DB 6; Length 854;
Best Local Similarity 100.0%; Pred. No. 3e-201;
Matches 854; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCAGGCCCAAGCCCTGTACCCGCGGTGGGGCCTCAGCTCTCGGCGATGGGGCGCT 60
DB 1 GCCAGGCCCAAGCCCTGTACCCGCGGTGGGGCCTCAGCTCTCGGCGATGGGGCGCT 60
QY 61 CCGCGCGGCTGCTGCGAGCGGTGATCATGAGGGGCCCGGGGCTCGGGCAAGGGCACCGTGT 120
DB 61 CCGCGCGGCTGCTGCGAGCGGTGATCATGAGGGGCCCGGGGCTCGGGCAAGGGCACCGTGT 120
QY 121 CGTCGCGCATCTACACACTTCGAGCTGAAAGCACCTCTCCAGCGGGGACCTGTCGCGG 180
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QY 841 TTATATTACTTTTA 854
DB 841 TTATATTACTTTTA 854

RESULT 2
AR094188
LOCUS AR094188 854 bp DNA linear PAT 08-SEP-2000
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DEFINITION Sequence 2 from patent US 6001624.
ACCESSION AR094188
VERSION AR094188.1 GI:10020933
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 854)
AUTHORS Hillman, J. L. and Shah, P.
TITLE Mitochondrial adenylate kinase
JOURNAL Patent: US 6001624-A 2 14-DEC-1999;
FEATURES
source 1. .854
/organism="unknown"
BASE COUNT 230 a 213 c 211 g 197 t 3 others
ORIGIN
Query Match 99.6%; Score 851; DB 6; Length 854;
Best Local Similarity 100.0%; Pred. No. 3e-201;
Matches 854; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCAGGCCCAAGCCCTGTACCCGCGGTGGGGCCTCAGCTCTCGGCGATGGGGCGCT 60
DB 1 GCCAGGCCCAAGCCCTGTGTACCCGCGGTGGGGCCTCAGCTCTCGGCGATGGGGCGCT 60
QY 61 CCGCGCGGCTGCTGCGAGCGGTGATCATGAGGGGCCCGGGGCTCGGGCAAGGGCACCGTGT 120
DB 61 CCGCGCGGCTGCTGCGAGCGGTGATCATGAGGGGCCCGGGGCTCGGGCAAGGGCACCGTGT 120
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DB 121 CGTCGCGCATCTACACACTTCGAGCTGAAAGCACCTCTCCAGCGGGGACCTGTCGCGG 180
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DB 181 ACAACATGCTGGGGGACAGAAATTTGGGTGTAGCCAAAGCCTTCATGTACCAAGGA 240
QY 241 AACCTATCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
DB 241 AACCTATCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
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DB 301 AGTATAGCTGGGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
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DB 361 GAGCTTATCAGATCGACACAGTATGATTAACCTGATGTCCTTGAAGTCAATTAACAAC 420
QY 421 GCCTTACTGCTGCTGGAATTCATCCCGCAGTGGCCGATGATTAACATTTGAATTCACC 480
DB 421 GCCTTACTGCTGCTGGAATTCATCCCGCAGTGGCCGATGATTAACATTTGAATTCACC 480
QY 481 CTCCCAAACTGTGGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
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DB 541 ATAAACAGAGACGGTTATCAAGAGACTAAAGGCTTATGAAGACCAACAAAGNAGTCC 600
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DB 601 TGGNATATTACAGAAAAAAGGGGTGCTGGAACATTTCTCCGGAAACAGAAACCAACAAGA 660
QY 661 TTTGGCCCTATGATATATGCTTTCTCCACAACTAAAGTTCACAAAGAAAGCCGAAAGCTT 720
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QY 721 CAGTTACTCATGAGAGAAATGTGTACTATTATATAGTAAAGTGGGCAAACTCCTA 780
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QY 781 GTCCTGCATTAGAGAGCTGCTTTCTCTAGACTCTAGTATGATGAATCTTTGAAA 840
|||||
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QY 841 TTATATTACTTTTA 854
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Db 841 TTATATTACTTTTA 854
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BC013771 1667 bp mRNA linear PRI 07-SEP-2001
LOCUS BC013771
DEFINITION Homo sapiens, clone MGC:21124 IMAGE:4385034, mRNA, complete cds.
ACCESSION BC013771
VERSION BC013771.1 GI:15489347
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1667)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (04-SEP-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.ncl.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-rt@mail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: Villalobos, tmc.edu.
Villalobos, D.K., Luna, R.A., Hale, S.M., Huylk, S., Lu, X., Garcia,
A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,
Muzny, D.M., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAX Plate: 26 Row: 0 Column: 3
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 7023533.
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BASE COUNT 516 a 329 c 349 g 473 t
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Best Local Similarity 99.2%; Pred. No. 2.8e-197;
Matches 848; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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Db 186 GACAACATGCTGCGGGGACAGAAATGGCGGTGTTAGCAAGGCTTTCATTGACCAAGG 245
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QY 840 ATTATATTACTTTTA 854
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Db 846 ATTATATTACTTTTA 860
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LOCUS AK001951 1701 bp mRNA linear PRI 01-NOV-2002
DEFINITION Homo sapiens cDNA FLJ11089 f1s, clone PLAC1005305, highly similar
to GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10).
ACCESSION AK001951
VERSION AK001951.1 GI:7023533
KEYWORDS oligo capping; f1s (full insert sequence).
SOURCE Homo sapiens placenta cDNA to mRNA, clone_1lb:PLAC1
clone:PLAC1005305.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;


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RSQKASVMP"
BASE COUNT      803 a      503 c      549 g      787 t
ORIGIN
Query Match      97.8%; Score 835.2; DB 9; Length 2642;
Best Local Similarity 99.2%; Pred. No. 2,9e-197;
Matches 848; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
QY 1 GCCANCCCAAGCCCTGTGACCCGGCGGTG-GGGCTCAGTCTGCGGCATGGGGCG 59
DB 90 GGCAGAGCCAAAGCCCTGTGATCCCGCGGTGCGGCTCAGTCTGCGGCATGGGGCG 149
QY 60 TCCGCGCGCTGCTGCGAGCGGTGATCATGGGGCGCGGCTCGGGCAAGGACCGTG 119
DB 150 TCCGCGCGCTGCTGCGAGCGGTGATCATGGGGCGCGGCTCGGGCAAGGACCGTG 209
QY 120 TCGTGGCGATCACTACACTTGGAGTGAACACCTCTCCAGCGGGGACCTGCTCCG 179
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QY 360 AGAGCTTATCAGATGACACAGATTAACCTGAATGCGCTTGAAGTCATTAACAA 419
DB 450 AGAGCTTATCAGATGACACAGATTAACCTGAATGCGCTTGAAGTCATTAACAA 509
QY 420 CGGCTTACGTCTGCTGATTCATCCCGCAGTGGCCGAGTATTAACATTAAC 479
DB 510 CGGCTTACGTCTGCTGATTCATCCCGCAGTGGCCGAGTATTAACATTAAC 569
QY 480 CCTCCCAAAACGTGGGCAATGATGACTGAGGAGGCGCTCTCAATTCAGCTGAGAT 539
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DB 630 GATTAACAGAGAGGTTTCAAGAGACTAAAGCTTATGAAAGCAACCAAGNAGTC 689
QY 600 CTGAGNATATTTACAGAAAAAGGGGTGCGAAATTTCTCCGGAACAGAACCAAG 659
DB 690 CTGAGNATATTTACAGAAAAAGGGGTGCGAAATTTCTCCGGAACAGAACCAAG 749
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QY 720 TCAGTACTCATGAGAGAAATGTGTAACTATTAAATAGTAGGCAACCTCTCT 779

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DB 810 TCAGTACTCATGAGAGAAATGTGTAACTATTAAATAGTAGGCAACCTCTCT 869
QY 780 AGTCTTGCATTTAGAGCTGCTTTTCTTAAGCTTCTAGATGATGAATTTTGAAA 839
DB 870 AGTCTTGCATTTAGAGCTGCTTTTCTTAAGCTTCTAGATGATGAATTTTGAAA 929
QY 840 ATTATATTACTTTTA 854
DB 930 ATTATATTACTTTTA 944

RESULT 6
LOCUS BD012403 2394 bp DNA linear PAT 02-AUG-2002
DEFINITION Novel genes encoding adenylate kinase 3(AK3) like proteins.
ACCESSION BD012403
VERSION BD012403.1 GI:22092592
KEYWORDS WO 0109346-A/1.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 2394)
REFERENCE
AUTHORS Ota,T., Isogai,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S.,
Nishikawa,T., Makamatsu,A., Nagai,K., Otsuk,T., Ihara,S., Nakee,H.,
Nishikawa,T. and Kimura,K.
Novel genes encoding adenylate kinase 3(AK3) like proteins
Patent: WO 0109346-A 1 08-FEB-2001;
HELIX RESEARCH INSTITUTE,TOSHIO OTA,TAKAO ISOGAI,KOJI HAYASHI,AORU
SAITO, JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI
MAKAMATSU, KEIICHI NAGAI,TETSUJI OTSUKI,SHIGEO IHARA,HIROKI NAKAE,
ETSUO NISHIKAWA, KOICHI KIMURA
OS Homo sapiens (human)
PN WO 0109346-A/1
PD 08-FEB-2001
PE 28-JUL-2000 WO 2000JP005066
PR 29-JUL-1999 JP 99P 248036,27-AUG-1999 JP 99P 300253 PR
11-JAN-2000 JP 00P 118776,18-OCT-1999 US 60/159590 PR
17-FEB-2000 US 60/183322
PI TOSHIO OTA,TAKAO ISOGAI,KOJI HAYASHI,KAOBU SAITO, PI JUNICHI
YAMAMOTO,
PI SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI MAKAMATSU,KEIICHI NAGAI, PI
TETSUJI OTSUKI,
PI SHIGEO IHARA,HIROKI NAKAE,TETSUO NISHIKAWA,KOICHI KIMURA PC
C12N15/54,C12N9/12,C12N1/21,C12P21/02,C07K16/40,C12Q1/68, PC
C12M1/00,
PC A61K45/00,A61P3/00,A61P25/00,A61P21/00,G01N33/566,G01N33/50,
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Matches 816; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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DB 1 CTCAGTCTGCGGCGCATGCGGGCGTCCGCGGCTGCTGCGAGCGGTGATCATGGGGCCC 60
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VERSION	AB021870.1	GI:6518532
KEYWORDS	h3k31alpha; adenylate kinase 3 alpha.	
SOURCE	Homo sapiens liver cDNA to mRNA.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	
AUTHORS	1 Noma, T., Fujisawa, K., Yamashiro, Y., Shinohara, M., Nakazawa, A., Condo, T., Ishihara, T. and Yoshinobu, K.	
TITLE	Structure and expression of human mitochondrial adenylate kinase targeted to the mitochondrial matrix	
JOURNAL	Biochem. J. 358 (Pt 1), 225-232 (2001)	
MEDLINE	21378190	
REFERENCE	2 (bases 1 to 684)	
AUTHORS	Noma, T.	
TITLE	Direct Submission	
JOURNAL	Submitted (25-DEC-1998) Takafumi Noma, Yamaguchi University School of Medicine, Department of Biochemistry, 1144 Kogushi, Ube, Yamaguchi 755-8505, Japan (E-mail: tnomapo.cc.yamaguchi-u.ac.jp, Tel.:81-836-42-2215, Fax:81-836-22-2315)	
FEATURES		

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BASE COUNT	186 a 179 c 173 g 146 t
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QY	291	AATCTCACCCAGTATAGCTGGCTGTGGATGGTTTTCCAAAGAACCTTCCACAGGCGAA	350		
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QY	351	GGCCTAGATAGAGCTTTATCAGTCGACACAGTATTAACTGAATGTGCCCTTTGAGGTC	410		
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QY	711	CAGAAAGCTTCAGTTACTCCATGA	734
Db	661	CAGAAAGCTTCAGTTACTCCATGA	684

RESULT 10.	
LOCUS	AF183419
DEFINITION	AF183419 Homo sapiens GTP:AMP phosphotransferase mRNA, complete cds; nuclear gene for mitochondrial product.
ACCESSION	AF183419
VERSION	AF183419.1 GI:9963776
KEYWORDS	.
SOURCE	Homo sapiens.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 1539)
AUTHORS	Li,Y., Peng,Y., Jiang,Z., Gu,W., Han,Z. and Chen,Z.
TITLE	A novel gene expressed in human pheochromocytoma
JOURNAL	Unpublished 2 (bases 1 to 1539)
REFERENCE	Peng,Y., Gu,W., Huang,C., Xu,S., Han,Z., Fu,G. and Chen,Z.
AUTHORS	Direct Submission
TITLE	Submitted (03-SEP-1999) Chinese National Human Genome Center at
JOURNAL	

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RESULT 11			
AK098205			
LOCUS			
DEFINITION	Homo sapiens CDNA FLJ40886 fls, clone UTERU2000663, highly similar		
ACCESSION	to GTR:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (BC 2.7.4.10).		
VERSION	AK098205.1 GI:21758171		
KEYWORDS	Oligo capping; fls (full insert sequence).		
SOURCE	Homo sapiens uterus CDNA to mRNA, clone_1lb:UTERU2		
	clone:UTERU2000663.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1		
	Oshima,A., Takahashi-Fujii,A., Tanase,T., Imose,N., Takeuchi,K.,		
	Arita,M., Musashino,K., Yuuki,H., Hara,H., Sugiyama,T., Irie,R.,		
	Osutuki,T., Saito,H., Makamatsu,A., Ishii,S., Yamamoto,J., Isono,Y.,		
	Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H.,		
	Masuno,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K.,		
	Wagatsunuma,M., Murakawa,K., Kanehori,K., Sugiyama,A., Kawakami,B.,		
	Suzuki,Y., Sugano,S., Nagahari,K., Masuno,Y., Nagai,K. and		
	Isoqai,T.		
TITLE	NEDO human cDNA sequencing project		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 3008)		
AUTHORS	Isoqai,T. and Yamamoto,J.		
TITLE	Direct Submission		
JOURNAL	Submitted (04-JUL-2002) Takao Isoqai, FLJ Project(HRI Team); 2-6-7		
	Kazuo-Kamatarei, Kizatzu, Chiba 292-0812, Japan		
	(E-mail:genomic@hri.co.jp, Tel:81-338-52-3975, Fax:81-338-52-3986)		
	NEDO human cDNA sequencing project supported by Ministry of		
	Economy, Trade and Industry of Japan; cDNA full insert sequencing;		
	Research Association for Biotechnology (RAB); cDNA library		
	construction; Helix Research Institute (HRI) (supported by Japan		
	key Technology Center etc.); 5'- & 3'-end one pass sequencing; RAB,		
	HRI, and Biotechnology Center.)		

Evaluation: clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.					
FEATURES	source	Location/Qualifiers			
		.3008 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="UTERU000663" /tissue_type="uterus" /clone_id="UTERU2" /note="Cloning vector: pMEI8SFL3"			
BASE COUNT	980 a	542 c	622 g	864 t	
ORIGIN					
Query Match	76.5%;	Score 653;	DB 9;	Length 3008;	
Best Local Similarity	99.7%;	Pred. No. 7.4e-152;			
Matches 653;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;	
OY	200	AGAAATTGGCGGTTCGATGCCAAGCGCTTTCATTTACCAAGGAACACTCATCCAGATGATGT	259		
Db	1568	AGAAAATTGGCGGTTCGATGCCAAGCGCTTTCATTTACCAAGGAACACTCATCCAGATGATGT	1627		
OY	260	CATGACTCGGCGTGCGCCTTCATGAGCTGAAAAAATCTCACCCAGTAATGACCTGGCTGTGGA	319		
Db	1628	CATGACTCGGCGTGCGCCTTCATGAGCTGAAAAAATCTCACCCAGTAATGACCTGGCTGTGGA	1687		
OY	320	TGGTTTTCCAAAGACACTTCCACAGGCAGAAAGCCCTAGATGAGCTTATCAGATGCACAC	379		
Db	1688	TGGTTTTCCAAAGACACTTCCACAGGCAGAAAGCCCTAGATGAGCTTATCAGATGCACAC	1747		
OY	380	AGTGAATTAAACCGATGATGCCCCCTTTGAGGTCTATAACAAGCCCTTACTGGTCGGTGAT	439		
Db	1748	AGTGAATTAAACCGATGATGCCCCCTTTGAGGTCTATAACAAGCCCTTACTGGTCGGTGAT	1807		
OY	440	TCATCCCGCCAGATGGCCGAGTCTATACATGTAATTCACACCTCCCAAACCTGTGGCAT	499		
Db	1808	TCATCCCGCCAGATGGCCGAGTCTATACATGTAATTCACACCTCCCAAACCTGTGGCAT	1867		
OY	500	TGATGACCTGACTGGGGAGCCTCTCATTCACGCGTAGATGATTAACCAGAGCGTTAT	559		
Db	1868	TGATGACCTGACTGGGGAGCCTCTCATTCACGCGTAGATGATTAACCAGAGCGTTAT	1927		
OY	560	CAAGGACTTAAAGGCTTTGTAAGAACCAAAAGCAGCTCCGNAATTTACCGAATAAA	619		
Db	1928	CAAGGACTTAAAGGCTTTGTAAGAACCAAAAGCAGCTCCGNAATTTACCGAATAAA	1987		
OY	620	AGGGGTGCTGGAACATTTCTCCGAAACAGAACCAGAAATTTGGCCCTATGATATGC	679		
Db	1988	AGGGGTGCTGGAACATTTCTCCGAAACAGAACCAGAAATTTGGCCCTATGATATGC	2047		
OY	680	TTTCTTACAACTAAAGTTCCACAAAGAGCCAGAAAGCTTCAGTTACTCCATGAGAGA	739		
Db	2048	TTTCTTACAACTAAAGTTCCACAAAGAGCCAGAAAGCTTCAGTTACTCCATGAGAGA	2107		
OY	740	AATGCTGTACTATTATATAGTAAGATGGGCAAACTCTAGTCTCTGCATTTAGAACT	799		
Db	2108	AATGCTGTACTATTATATAGTAAGATGGGCAAACTCTAGTCTCTGCATTTAGAACT	2167		
OY	800	GCTTTTCCTAAGACTTCTAGTATGATGAATCTTTGAAAATTTATATTAAGTTTAA	854		
Db	2168	GCTTTTCCTAAGACTTCTAGTATGATGAATCTTTGAAAATTTATATTAAGTTTAA	2222		
RESULT 12					
BOVPIKAMP					
LOCUS					
DEFINITION	Bovine mitochondrial GTP:AMP phosphotransferase mRNA, complete cds.	3631 bp	mRNA	linear	MAM 27-Apr-1993
ACCESSION	M25757				
VERSION	M25757.1	GI:163522			
KEYWORDS	GTP:AMP phosphotransferase; adenylate kinase.				
SOURCE	Bovine liver; cdna to mRNA, clones lambda-bcaK3-(1-1.2-2-2-1-2-8-3-5-3-9-2-3-2-7).				
ORGANISM	EusayOta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Balaenoptera; Cetacea; Mammalia; Artiodactyla; Bovidae; Bos taurus				

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
Bovidae; Bovinae; Bos.
1 (bases 1 to 3631)
Yamada, M., Shajibhan, M., Tanabe, T., Kishi, F. and Nakazawa, A.
Cloning and characterization of cDNA for mitochondrial GTP:AMP
phosphotransferase of bovine liver
J. Biol. Chem. 264 (32), 19192-19199 (1989)
JOURNAL 90037053
MEDLINE 2478555
COMMENT Draft entry and computer-readable sequence for [1] kindly provided
by M. Yamada, 27-JUN-1989.

FEATURES
Source location/Qualifiers
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/organism="Bos taurus"
/db_xref="taxon:9913"
139..822
/note="GTP:AMP phosphotransferase (EC 2.7.4.10)"
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/codon_start=1
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/db_xref="GI:163528"
/translation="MGASARLLRAAIMGAPSGKGVSSRIKHPKELKHLSSGDLRL
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REDDEPETVVKRLKAYEAOEPEVLEYRKKGVLTEFSGTEINKIWPVYAFLOTXLPQ
RSQETSTVP"

BASE COUNT 1074 a 716 c 760 g 1081 t
ORIGIN 135 bp upstream of PstI site.

Query Match 71.9% Score 613.6; DB 4; Length 3631;
Best Local Similarity 85.9%; Pred. No. 5e-142;
Matches 704; Conservative 0; Mismatches 111; Indels 5; Gaps 2;

QY 35 GCCTCAGTCTGCGCCATGGGGCGCTCGCGGGCTGCTGACGAGCGGTATCATGGGGC 94
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QY 95 CCGGGCTGGGCAAGGAGGACCGTCTGCTGGGCGCATCATACACTTGGAGCTGAAGA 154
DB 183 GCGGGCTCTGGCAAGGACCGTCTGCTGGGCGCATCAACACTTGGAGCTGAAGA 242
QY 155 CCTCTCAGCGGGGACCTCTCGGAGCAACATGCTGCGGGCAGACGAATGGCGCTTT 214
DB 243 CCTCTCAGCGGGGACCTCTCAGAGATATATGCTCGGGCAGACGAATGGCTTTT 302
QY 215 AGCCAAAGCTTTCATTGACCAAGGAACATCCAGATGATGTCATGCTCGCGTGC 274
DB 303 AGCCAAAGCTTTCATTGACCAAGGAACATCCAGATGATGTCATGCTCGGTGGT 362
QY 275 CCTGATGAGTGAAGAAATCTCACCAGATAGCTGGCTGTGGATGTTTCCAAAGAC 334
DB 363 CCTGATGAGTGAAGAAATCTCACCAGATAGCTGGCTGTGGATGTTTCCAAAGAC 422
QY 335 ACTTCCACAGGACGACCCCTAGATGAGCTTATGATGACAGACAGTGAATTAACCTGAA 394
DB 423 ACTTCCAGGACGACCCCTGATAGAGCTTATGATGACAGACAGTGAATTAACCTGAA 482
QY 395 TGTGCCCTTTGAGTCAATTAACAACGCGCTTACTGCTGCTGGATTCATCCGCGAGTGG 454
DB 483 CGTGCGCTTTGAGTCAATTAACAACGCGCTTACTGCTGCTGGATTCATCCGCGAGTGG 542
QY 455 CGGAGCTTAACTGATTAACCTTCCCAAACTGGGGCATGATGATGATGATGATGATGATG 514
DB 543 CGGAGCTTAACTGATTAACCTTCCCAAACTGGGGCATGATGATGATGATGATGATGATG 602
QY 515 GAGAGCTTCACTGAGCGTGAAGATGATTAACAGAGAGGTTATCAAGAGATGAAGGC 574
DB 603 GAGAGCTTCTTTCACGCGTGAAGATGATTAACAGAGAGGTTATCAAGAGATGAAGGC 662
QY 575 TTATGAAGACCAAGAACAGTCTCTGATATTAACAGAGAGAGAGAGAGAGAGAGAGAGAG 634
DB 663 TTATGAAGACCAAGAACAGTCTCTGATATTAACAGAGAGAGAGAGAGAGAGAGAGAGAG 722
QY 635 ATTCTCCGAGACAGAACAGATTTGGCGCTATGATATGCTTCTTCAAACTGA 694

DB 723 ATTCCTGGAACAGAAACCAACAGATGCGGCACATGATATATGCTTCTCAACAAACA 782
QY 695 AGTCCACAAAGAGCCAGAAAGCTTCACTATCTCATGAGAGAAATGTGTACTAT 754
DB 783 ACTTCCACAAAGAGCCAGAAAGATGATGATGATGATGATGATGATGATGATGATGATG 842
QY 755 TATAGTAGATGAGGCAACCTCTGCTGATGATGATGATGATGATGATGATGATGATGATG 814
DB 843 GAAGATGA---GCAACAGCTCTTCTCTTGTGATGATGATGATGATGATGATGATGATGATG 897
QY 815 TCTAGTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 854
DB 898 TCTGCGCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 937

RESULT 13
AF417508
LOCUS AF417508 725 bp mRNA linear MM 26-SEP-2001
DEFINITION Oryctolagus cuniculus adenylate kinase 3 mRNA, complete cds.
ACCESSION AF417508
VERSION AF417508.1 GI:15778673
KEYWORDS
SOURCE
ORGANISM Oryctolagus cuniculus.
Oryctolagus cuniculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
1 (bases 1 to 725)
Brochiero, E., Coady, M.J., Klein, H., Laprade, R. and Lapointe, J.Y.
Activation of an ATP-dependent K⁺ conductance in Xenopus oocytes
by expression of adenylate kinase cloned from renal proximal
tubules
JOURNAL Biochim. Biophys. Acta 1510 (1-2), 29-42 (2001)
MEDLINE 21240235
PUBMED 11342145
REFERENCE 2 (bases 1 to 725)
AUTHORS Brochiero, E. and Lapointe, J.Y.
TITLE Direct Submission
JOURNAL Submitted (10-SEP-2001) Department of Physiology, Université de
Montréal, PO Box 6128, Succursale Centre-ville, Montréal, QC H3C
3J7, Canada

FEATURES
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/tissue_type="renal proximal tubule"
1..684
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BASE COUNT 196 a 188 c 201 g 140 t
ORIGIN

Query Match 67.2% Score 573.6; DB 4; Length 725;
Best Local Similarity 87.9%; Pred. No. 3.8e-132;
Matches 624; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 51 ATGGGGCGCTCGCGCGCTGCTGAGAGCGGATGATGAGGCGCGCGCGCGCGCGCGCGCGCGCG 110
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QY 111 GGCACCGTCTGCTCGCGCTGCTGAGAGCGGATGATGAGGCGCGCGCGCGCGCGCGCGCGCG 170
DB 61 GGCACCGTCTGCTCGCGCTGCTGAGAGCGGATGATGAGGCGCGCGCGCGCGCGCGCGCGCG 120
QY 171 CTGCTCCGGGACACATGCTGCGGGGACAGAAATTTGGCGGTGTAGCCAAAGCTTTCAAT 230

D	b		121	CTGCGTGGCAGACATCTCTGGAGGCACAGAAATTGGTTGTGTATGCCAAGACTTCATT	180
O	y		231	GACCAGGGAATCTCATCCAGATGATGTCAATGACTGGCCCTTCATGAGCTGAAA	290
D	b		181	GATCAAGGAGAGCTCATTCAGATGATGTCAATGACTGGCCCTTCATGAGCTGAAA	240
O	y		291	AATCTCACCCAGATATAGCTGGCTGTGGATGTGTTTTCCAAGGACACTTCACAGGCAGA	350
D	b		241	AATCTCACCCAGGACAGCTGGCTGTGGATGTGTTTTCCAAGGACACTTCACAGGCAGA	300
O	y		351	GCCCTAGATAGAGCTTATCATGATGCACACAGATTAACCTGAATGTGCCCTTGAGGTC	410
D	b		301	GCCCTGGACAGAGCTTATCATGATGCACACCGTGAATTAACCTGAATGTGCCCTTGAGGTC	360
O	y		411	ATTTAACACAGCGCTTACTGCTCGCTGGATTCATCCCCGACAGTGGCCGATGCTATAACAT	470
D	b		361	ATTTAGCAAGCGCTTACTGCTCGCTGGATTCATCCCCGACAGTGGCCGATGCTATAACAT	420
O	y		471	GAATTCAACCTCCCAAACCTGTGGGCAATTGATGACCTGACTGGGAGCCTCTCAATCAG	530
D	b		421	GAGTTCAACCTCCCAAACCTGTGGGCAATTGATGACCTGACTGAGGAGCCTCTCAATCAG	480
O	y		531	CGTGGATGTATTAACCGACAGCGTTTCAAGAACACTAAAGGCTTATGAGAACCAACA	590
D	b		481	CGTGGAGCGACAAAGCCAGAGACGGTCAATCAAGACATGAAGGCAATGAGGCTTCAACG	540
O	y		591	AAGNAGTCTGTGNATATTATACAGAAAAAGGGGTGTGAAACATTTCTCCGCAACAGA	650
D	b		541	GAGCGGCTCTGTGATTAATACCGGAAAAAGGGGTGTGAAACATTTCTCTGGAACAGAA	600
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D	b		601	ACCATATAGATTCGGGCCCAAGCTATATGCTTTCTTACAACCAAGATTTCCAGAACCAAC	660
O	y		711	CAGAAAGCTTCAATTCATCCATGAGAGAAATGTGTGAATTAATTAATG	760
D	b		661	CAGAAAGACTCGTCTACTTCATGAGAGAAACGACATCACACAGGAAG	710
RESULT 14					
BC016432					
L	OCUS		BC016432	1850 bp	mRNA linear ROD 07-AUG-2002
D	EFINITION		Mus musculus,	adenylate kinase 3 alpha like,	clone MGC:25636
			IMAGE:4217820,	mRNA, complete cds.	
A	CCESION		BC016432		
V	ERSION		BC016432.1	GI:16741172	
K	EYWORDS				
S	OURCE				
			house mouse.		
			Mus musculus		
			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
			Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
R	EFERENCE				
T	ITL				
J	OURNAL				
			Strausberg,R.		
			Submitted (31-OCT-2001)	National Institutes of Health, Mammalian	
			Gene Collection (MGC), Cancer Genomics Office, National Cancer		
			Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,		
			USA		
			NIH-MGC Project URL:	http://mgc.ncl.nih.gov	
			Contact: MGC help desk		
			Email: cgapbs@mail.nih.gov		
			Tissue Procurement: Jeffrey E. Green, M.D.		
			cDNA Library Preparation: Life Technologies, Inc.		
			cDNA Library Arrayed by: Baylor College of Medicine Human Genome		
			Sequencing Center		
			Center code: BCM-HGSC		
			Web site: http://www.hgsc.bcm.tmc.edu/cdna/		
			Contact: amge@bcm.tmc.edu		
			Gunaratne, P.H., Garcia, A.M., Lu, X., Huylk, S.W., Hale, S.M.,		
			Yoon, V.S., Kowals, C.R., Martini, R.G., Muzny, D.M.,		
			Richards, S., Gibbs, R.A.		

Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/ILN at: <http://image.llnl.gov>
Series: IRM Plate: 31 Row: b Column: 19
This clone was selected for full length sequencing because it passed the following selection criteria: GeneScan gene prediction, similarity but not identity to protein.

FEATURES
source

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/map="FVB/N"
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CDS

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Query Match	67.18;	Score 573.4;	DB 10;	Length 1850;
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Matches 634; Conservative 0; Mismatches 104; Indels 0; Gaps 0;
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QY	61	CCGCGGGGCTGTCTCGAGAGCGGTATCATGTGGGGGCCCGGGGCTCGGGCAAGGGCACCGTGT	120
Db	86	CGGGGGCGGCTGTCTCGGCGCGCTGTATCATGTGGGGGCCCGGGGCTCGGGCAAGGGCACCGTGT	145
QY	121	CGTGGCGCATACATACACACTGTGAGGTGAAGACACCTCCAGCGGGGGACCTGTCTCGGG	180
Db	146	CGTACGCATATACCAAACTCTGAGCTGAAGACACCTCTCCAGCGGGGACCTGTCTCGGC	205
QY	181	ACAACATGTCTGCGGGGCGACAGAAATTTGGCGTTTAGGCCAAGGCTTTTATTGACCAAGGA	240
Db	206	AGAACATGTCTGACAGGCGACAGAAATTTGGTGTGTGGCGAAGACTTTCATTGACCAAGGA	265
QY	241	AACATCATCCAGATGATGTATCTAGCTGGCGTGGCCCTTCATGAGCTGAATAATTTCACCC	300
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QY	481	CTCCCAAAACGTGTGGCATGTGATGACCTGCACTGGGAGAGCTCTCATTTACAGGTGAGATG	540
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 Db 746 CTGTTACTCTGAGAG 763
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 DEFINITION IMAGE:5007578, mRNA, complete cds.
 ACCESSION BC019174
 VERSION BC019174.1 GI:17512427
 KEYWORDS MGC.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 1860)
 Strausberg, R.
 Direct Submission
 Submitted (07-DEC-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: http://mgc.nci.nih.gov
 Contact: MGC help desk
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: http://www.nisc.nih.gov/
 Contact: nisc.mgc@nih.gov
 Akhtar, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
 Blakesley, R.W., Bouffard, G., Breen, K., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, F., Latic, P., Legaspi, R.,
 Maduro, Q.D., Mastello, C., Maskell, B., Mastrian, S.D., McCloskey, J.C.,
 McDowell, J., Pearson, R., Stantrilop, S., Thomas, P.J., Touchman, J.W.,
 Turgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
 Young, A., Zhang, L.-H. and Green, E.D.
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
 Series: IMAX Plate: 39 Row: e Column: 2
 This clone was selected for full length sequencing because it
 passed the following selection criteria: Genomescan gene
 prediction, similarity but not identity to protein.
 Location/Qualifiers
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 TTOKASVMP"
 BASE COUNT 530 a 467 c 440 g 423 t
 ORIGIN

Query Match 67.1%; Score 573.4; DB 10; Length 1860;
 Best Local Similarity 85.9%; Pred. No. 4.8e-132;
 Matches 634; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 1 GCCANCCCAAGCCCTGTACCCGCGGCTGAGTCTGCGCCATGCGGCGCT 60
 Db 77 GGCACAGCCACAGACAGCGGTCTGCGACCTGGACACCGCCAGCCATGCGGCGCT 136
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 Db 137 CCGGGCGCTGCTGCGCGCGGTGATCATGGGGCCCGGCTCGGGCAAGGCGACCGGT 196
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 Db 197 CGTACAGCATACCAAACTCTGAGCTGAACACCTCTCCAGCGGGACCTCTCCGG 256
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 Db 257 ACACATGCTGGAGGCAAGAAATGGCTTTAGCCAAAGCTTTCATGACCAAGGA 316
 QY 241 AACTATCCCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
 Db 317 ACCTATCCCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 376
 QY 301 AGTATAGCTGCTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
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 Db 497 GCCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 556
 QY 481 CTCCTCAAACTGTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
 Db 557 CTCCTCAAACTGTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 616
 QY 541 ATAAACCAAGAGCGTTATCAAGAGACTAAGGCTTATGAACCAACCAAGNCAAGTCC 600
 Db 617 ACAAACAGAGACAGTATCAAGAGACTAAGGCTTATGAACCAACCAAGNCAAGTCC 676
 QY 601 TGGNATATTACCAAGAAAAAGGGGTCTGAAACATTTCTCCGAAACAGAAACCAACAAGA 660
 Db 677 TCGAGTATTACCAAGAAAAAGGGGTCTGAAACATTTCTCGAACAAGAAACCAACAAGA 736
 QY 661 TTTGGCCCTATATATGCTTTCTCAACAACTAAGTCCACAAAGAGCCAGAAAGCTT 720
 Db 737 TCTGGCCCACTATACCTCTCTCAACAGAAAGTCCAGAAACTACCAAAAGGCGCT 796
 QY 721 CAGTTACTCTAGAGAG 738
 Db 797 CTGTTACTCTGAGAG 814

Search completed: March 19, 2003, 13:08:16
 Job time : 31308 secs

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: March 18, 2003, 19:51:08 ; Search time 253 Seconds
(without alignments)
7601.607 Million cell updates/sec

Title: US-10-006-190-2

Perfect score: 854
Sequence: 1 GCCAGCCCCAAGCCCTGCT.....TGAAATATATATTACTTTTA 854

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	851	99.6	854	19	AAV68223	Human mitochondria
2	835.2	97.8	1701	22	AAH14909	Human cDNA sequenc
3	835.2	97.8	1751	19	AAV59568	Human secreted pro
4	835.2	97.8	2642	22	AAH14427	Human cDNA sequenc
5	835.2	97.8	2765	22	AAH33296	Human colon cancer
6	820	96.0	2041	22	ABA08570	Human secreted pro
7	820	96.0	2432	22	AAI58841	Human polynucleoti
8	816.8	95.6	2421	22	AAI58055	Human polynucleoti
9	816	95.6	2394	22	AAH14215	Human cDNA sequenc

10	816	95.6	2394	22	AAH47197	Human adenylate kinase
11	729.8	85.5	751	21	AAH60582	Human mitochondria
12	691.4	81.0	733	21	AAC38376	Human colon Cancer
13	659.2	77.2	851	22	AAH06376	Human CDNA clone (
14	595.2	69.7	639	22	AH05788	Human CDNA clone (
15	578.6	67.8	603	22	AAH07675	Human CDNA clone (
16	571.6	66.9	684	21	AAH60585	AK3 nucleotide seq
17	392.2	45.9	2238	22	AA57219	CDNA encoding nove
18	366	42.9	881	22	AA194359	Human neuroblastom
19	255	29.9	1707	24	ABN97254	Gene #3752 used to
20	255	29.9	1707	24	ABL64778	Lung cancer relate
21	255	29.9	1707	24	ABL65257	Lung cancer relate
22	255	29.9	1707	24	ABL66518	Lung cancer relate
23	255	29.9	1707	24	ABL68575	Kidney cancer rela
24	241	28.2	787	22	AA197232	Human neuroblastom
25	241	28.2	1947	22	AA105747	Human reproductive
26	241	28.2	8153	22	AA105749	Human reproductive
27	241	28.2	8163	22	AAK84484	Human immune/hae
28	226.4	26.5	912	22	AA108837	Human kinase (PKIN
29	190.2	22.3	699	23	AB114477	Drosophila melanog
30	190.2	22.3	3454	23	AB114476	Drosophila melanog
31	168	19.7	568	24	ABK38942	CDNA encoding lung
32	131.4	15.4	78845	21	AAAB1463	N. meningitidis pa
33	131.4	15.4	349980	21	AAAF1608	Neisseria meningit
34	119.2	14.0	645	23	AA553274	Haemophilus influe
35	117.6	13.8	645	23	AA555982	Salmonella typhi D
36	111.2	13.0	648	23	AA554207	Pseudomonas aerugi
37	108.4	12.7	1023	21	AA537085	Arabidopsis thalia
38	107.2	12.6	89047	22	AAAF8547	Genomic fregment #
39	106.8	12.5	1017	21	AAAF9022	Arabidopsis thalia
40	104	12.2	894	24	ABN98716	Arabidopsis thalia
41	102.8	12.0	645	23	AA553899	Klebsiella pneumon
42	101.2	11.9	637	23	ABK7752	Bacillus clausii g
43	101.2	11.9	2031	24	ABK78931	Bacillus clausii g
44	101	11.8	684707	24	AB067196	Listeria innocua C
45	101	11.8	3011208	24	AB069245	Listeria innocua C

ALIGNMENTS

	RESULT 1
XX	AAV68223
XX	ID AAV68223 standard; cDNA; 854 BP.
XX	AC
XX	AAV68223:
XX	DT
XX	29-JAN-1999 (first entry)
XX	Human mitochondrial adenylate kinase gene.
XX	ss; human; mitochondrial; adenylate kinase; therapeutic;
XX	KW neurological disorder; Alzheimer; Huntington; epilepsy; cancer;
XX	KW neural; inflammation; immune.
XX	OS
XX	Homo sapiens.
XX	Key
XX	Location/Qualifiers
XX	FT CDS
XX	51..734
XX	/tag= a
XX	/product= "Mitochondrial adenylate kinase"
XX	/transl_except= (pos:594..596,aa:Xaa)
XX	/transl_except= (pos:603..605,aa:Xaa)
XX	/note= "Xaa is unspecified"
XX	PN MO9844124-AI.
XX	PD
XX	08-OCT-1998.
XX	PE
XX	30-MAR-1998; 98MO-US06249.
XX	PR
XX	31-MAR-1997; 97US-0829027.
XX	

```
PA (INCY-) INCYTE PHARM INC.
XX
XX Hillman JL, Shah P;
XX WPI: 1998-557119/47.
XX P-PSDB: AAW81101.
XX
XX Human mitochondrial adenylate kinase, HMAK - useful e.g. to treat
XX neurological disorders such as Alzheimer's and screen for
XX antagonists for treatment of cancer or immunological disorders
XX
XX Claim 1, Fig 1: 63pp; English.
XX
XX The human mitochondrial adenylate kinase (HMAK) (854bp) gene encodes a
XX protein of 227 amino acids ) can be administered therapeutically,
XX especially by expressing encoding polypeptides, to treat neurological
XX disorders e.g. Alzheimer's disease, Huntington's disease, epilepsy. It
XX can be combined with a suitable carrier in pharmaceutical compositions,
XX which can be administered to treat such disorders. HMAK was shown to
XX have chemical and structural homology with adenylate kinase isozyme 3
XX (AK3) from cow, rat and human (92, 91 and 57 % identity respectively)
XX and was expressed in e.g. cancerous tissues, brain and neural tissues
XX and tissues involved in inflammation and the immune response.
XX Increased activity or expression was proposed to be associated with
XX cancer and immunological disorders, and decreased activity/expression
XX with the development of neurological disorders. Products of the above
XX invention may be used in the diagnosis and treatment of the above
XX diseases and disorders.
XX
XX Sequence 854 BP; 230 A; 213 C; 211 G; 197 T; 3 other;
XX
XX Query Match 99.6%; Score 851; DB 19; Length 854;
XX Best Local Similarity 100.0%; Pred. No. 5.2e-241;
XX Matches 854; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX 1 GCCAAGCCCAAGAGCCCTGTACCCGGCGGCTTCTGAGTCTGGCGCCATGGGGCGT 60
XX 1 GCCAAGCCCAAGAGCCCTGTACCCGGCGGCGGCTTCTGAGTCTGGCGCCATGGGGCGT 60
XX 61 CGCGCGGCGTGTGCTGAGCGGTGATCATGGGGGCCCGGGCTCGGCAAGGGACCGTGT 120
XX 61 CGCGCGGCGTGTGCTGAGCGGTGATCATGGGGGCCCGGGCTCGGCAAGGGACCGTGT 120
XX 121 CGTCGGGCATCACTACACTTTCGAGCTGAGCAACCTTCCAGCGGGGACCTGCTCCGG 180
XX 121 CGTCGGGCATCACTACACTTTCGAGCTGAGCAACCTTCCAGCGGGGACCTGCTCCGG 180
XX 121 CGTCGGGCATCACTACACTTTCGAGCTGAGCAACCTTCCAGCGGGGACCTGCTCCGG 180
XX 181 ACAACATGCTGGGGGCAAGAAATTTGGGCTTACCCAAAGGCTTTCATTTGACCAAGGGA 240
XX 181 ACAACATGCTGGGGGCAAGAAATTTGGGCTTACCCAAAGGCTTTCATTTGACCAAGGGA 240
XX 241 AACATATCCCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
XX 241 AACATATCCCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
XX 301 AATATAGCTGCTGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
XX 301 AATATAGCTGCTGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
XX 361 GAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
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XX 421 GCCTTACTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
XX 421 GCCTTACTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
XX 481 CTCGCAAAAGCTGTGGCATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
XX 481 CTCGCAAAAGCTGTGGCATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
XX 541 ATAAACGAGAGCGTATATCAAGAGCTTAAGGCTTATGAACCAACCAAGNCAAGTCC 600
XX |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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DB 601 TGGNATATTACAGAAAAAGGGGTGCTGGAACATTCTCGGAAACAGAAACCAACAGA 660
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DB 661 TTTGGCCCTATGTAATGCTTTCTTCAAACTAAAGTTCACAAAGAGCCAGAAAGCTT 720
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DB 721 CAGTTACTCATGAGGAGAAATGCTGTAATTAATTAAGTATGATGATGATGATGATGATGAT 780
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DB 781 GTCTTCGATTTGAAGCTCTTTCTTCAAGCTTCTAGATGATGATGATGATGATGATGATGAT 840
QY 841 TTATATTACTTTTA 854
DB 841 TTATATTACTTTTA 854

RESULT 2
AAH14909
ID AAH14909 standard; cDNA: 1701 BP.
XX
XX AAH14909;
XX
XX 26-JUN-2001 (first entry)
XX
XX Human cDNA sequence SEQ ID NO:12785.
XX
XX Human; primer: detection; diagnosis; antisense therapy; gene therapy; ss.
XX
XX Homo sapiens.
XX
XX EP1074617-A2.
XX
XX 07-FEB-2001.
XX
XX 28-JUL-2000; 2000EP-0116126.
XX
XX 29-JUL-1999; 99JP-0248036.
XX
XX 27-AUG-1999; 99JP-0300253.
XX
XX 11-JAN-2000; 2000JP-0118776.
XX
XX 02-MAY-2000; 2000JP-0183767.
XX
XX 09-JUN-2000; 2000JP-0241899.
XX
XX (HELI-) HELIX RES INST.
XX
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
XX WPI: 2001-318749/34.
XX
XX Primer sets for synthesizing polynucleotides, particularly the 5602
XX full-length cDNAs defined in the specification, and for the detection
XX and/or diagnosis of the abnormality of the proteins encoded by the
XX full-length cDNAs -
XX
XX Claim 8: SEQ ID 12785; 2537bp + CD ROM; English.
XX
XX The present invention describes primer sets for synthesizing 5602
XX full-length cDNAs defined in the specification. Where a primer set
XX comprises: (a) an oligo-dT primer and an oligonucleotide complementary
XX to the complementary strand of a polynucleotide which comprises one of
XX the 5602 nucleotide sequences defined in the specification, where the
XX oligonucleotide comprises at least 15 nucleotides; or (b) a combination
XX of an oligonucleotide comprising a sequence complementary to the
XX complementary strand of a polynucleotide which comprises a 5'-end
XX sequence and an oligonucleotide comprising a sequence complementary to a
XX polynucleotide which comprises a 3'-end sequence, where the
```

CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.

xx Sequence 1701 BP; 500 A; 348 C; 372 G; 481 T; 0 other;

Query Match 97.8%; Score 835.2; DB 22; Length 1701;

Best Local Similarity 99.2%; Pred. No. 3.5e-236;

Matches 848; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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DB 62 GGCAGGCCCAAGCCCTGTACCCGGGGGTG-GGGCTCAGCTCCGGCCATGGGGCG 121
OY 60 TCCGGCGGGCTCTCGGACGGGTGATCATGGGGCCCCGGGCTCGGCAAGGCGACCTG 119
DB 122 TCCGGCGGGCTCTCGGACGGGTGATCATGGGGCCCCGGGCTCGGCAAGGCGACCTG 181
OY 120 TCGTGGCGGATCATACACTTCGAGCTGGAAGCACCCTCCGACGGGGACCTCGCTCCGG 179
DB 182 TCGTGGCGGATCATACACTTCGAGCTGGAAGCACCCTCCGACGGGGACCTCGCTCCGG 241
OY 180 GACACATGCTCGGGGGCAGCAAAATTGGCTGTAGCCCAAGGCTTCATTGACCAAGG 229
DB 242 GACACATGCTCGGGGGCAGCAAAATTGGCTGTAGCCCAAGGCTTCATTGACCAAGG 301
OY 240 AAATCTATCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 299
DB 302 AAATCTATCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 361
OY 300 CAGTATAGCTGGCTGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 359
DB 362 CAGTATAGCTGGCTGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 421
OY 360 AGAGCTTATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 419
DB 422 AGAGCTTATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 481
OY 420 CGCTTACTGCTCGCTGATTCATCCCGCAGTGGCGAGTCTATTAACATTTGAATTCAC 479
DB 482 CGCTTACTGCTCGCTGATTCATCCCGCAGTGGCGAGTCTATTAACATTTGAATTCAC 541
OY 480 CCTCCCAAACTGTGGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 539
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DB 602 GATTAACAGAGACGGTTATCAAGAGACTAAAGGCTTATGAAGACCAACCAAGNAGTC 661
OY 600 CTGGNATATTACCAAAAAAGGGGTGCGAAACATTTCTCCGAAACAGAACCAACAG 659
DB 662 CTGGNATATTACCAAAAAAGGGGTGCGAAACATTTCTCCGAAACAGAACCAACAG 721
OY 660 ATTGGCCCTATGATATGCTTTCCACAACTAAAGTTCCCAAAAGGCCGAAGCT 719
DB 722 ATTGGCCCTATGATATGCTTTCCACAACTAAAGTTCCCAAAAGGCCGAAGCT 781
OY 720 TCAGTACTCATGAGAGAAATGTGTAACTATTATAGTAAAGTGGCAAACTCCG 779
DB 782 TCAGTACTCATGAGAGAAATGTGTAACTATTATAGTAAAGTGGCAAACTCCG 841
OY 780 AGTCTTGATTTAGAGGTGCTTTTCCTAAGACTTCTAGTATGATGATTTCTTGAAA 839

DB 842 AGTCTTGATTTAGAGGTGCTTTTCCTAAGACTTCTAGTATGATGATTTTGAAA 901
OY 840 ATTATATTACTTTTA 854
DB 902 ATTATATTACTTTTA 916
RESULT 3
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ID AAV59568 standard; DNA; 1751 BP.
XX
AC AAV59568;
XX
DT 06-JAN-1999 (first entry)
XX
DE Human secreted protein gene 58 clone HHHFN61.
XX
XX
KW Human: secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW immune system; aschma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
OS Homo sapiens.
XX
XX W09839448-A2.
XX
PD 11-SEP-1998.
XX
PF 06-MAR-1998; 98WC-US04493.
XX
PR 02-OCT-1997; 97US-0061060.
PR 07-MAR-1997; 97US-0038621.
PR 07-MAR-1997; 97US-0040161.
PR 07-MAR-1997; 97US-0040162.
PR 07-MAR-1997; 97US-0040163.
PR 07-MAR-1997; 97US-0040333.
PR 07-MAR-1997; 97US-0040334.
PR 07-MAR-1997; 97US-0040336.
PR 07-MAR-1997; 97US-0040626.
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PR 23-MAY-1997; 97US-0047589.
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PR	23-MAY-1997;	97US-0047612.
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PR	06-JUN-1997;	97US-0048964.
PR	06-JUN-1997;	97US-0048974.
PR	13-JUN-1997;	97US-0049610.
PR	08-JUL-1997;	97US-0051926.
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PR	22-AUG-1997;	97US-0056630.
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PR	22-AUG-1997;	97US-0056864.
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PR	22-AUG-1997;	97US-0056908.
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PR	22-AUG-1997;	97US-0056910.
PR	22-AUG-1997;	97US-0056911.
PR	05-SEP-1997;	97US-0057650.
PR	05-SEP-1997;	97US-0057669.
PR	05-SEP-1997;	97US-0057761.
PR	12-SEP-1997;	97US-0056785.
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Bednarik DP, Brewer LA, Carter KC, Duan R, Ehrens R, Endress GA,	
PI	Feng P, Fertile AM, Fischer CL, Florence KA, Greene JM, Hu JS;	
PI	Kyia H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA;	
PI	Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;	
XX		
DR	WPI: 1998-506364/43.	
XX	P-PSDB: AAM74788.	
PT	New isolated human genes and the secreted polypeptide(s) they encode	
PT	- useful for diagnosis and treatment of e.g. cancers, neurological	

Query Match	Best Local Similarity	Score	DB	Length
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		Pred. No. 3.5e-236		
		Mismatches 6; Indels 1; Gaps 1		
1 GCCAAGCCCAAGCCCTGGTACCGCGCGCGT-66GCTCAGTCTGCGGCCATGGGGGCG 59				
44 GGCAGAGCCAAAGCCCTGGTACCCCGCGCGTCCGGGCTCACTGCGGCCATGGGGGCG 103				
60 TCCGCGCGGCTCTCGAGCGGTGATCATGGGGGCGCGCGCTCGGGCAAGGGCACCGTG 119				
104 TCCGCGCGGCTCTCGAGCGGTGATCATGGGGGCGCGCGCTCGGGCAAGGGCACCGTG 163				
120 TCGTGGCGCATACTACACACTTCGAGCTGAAGCACACTCTCCAGCGGGGACTGCTCGG 179				
164 TCGTGGCGCATACTACACACTTCGAGCTGAAGCACACTCTCCAGCGGGGACTGCTCGG 223				
180 GACCAATGCTCTCGGGGCGCAGAAATTTGGCGGTTAGCCAAAGCTTTTCATTGACCAAGG 239				
224 GACCAATGCTCTCGGGGCGCAGAAATTTGGCGGTTAGCCAAAGCTTTTCATTGACCAAGG 283				
240 AAAGTATCCAGATGATGTCAATGATCGGCTGGCGCTTCATGAGCTGAAATATCTACC 299				
284 AAAGTATCCAGATGATGTCAATGATCGGCTGGCGCTTCATGAGCTGAAATATCTACC 343				
300 CAGTATAGCTGGCTGTGGATGGTTTTCCAAAGACACTTCCAGGAGCAAGCCCTAGAT 359				
344 CAGTATAGCTGGCTGTGGATGGTTTTCCAAAGACACTTCCAGGAGCAAGCCCTAGAT 403				
360 AGAGCTTATCAATGATGACACAGTGAATTAACCGAATGTGCCCTTGGAGTCTTTAAACA 419				
404 AGAGCTTATCAATGATGACACAGTGAATTAACCGAATGTGCCCTTGGAGTCTTTAAACA 463				
420 CGCCTTACTGCTCGTGATTCATCCCGCAGTGGCGCGAGTCTATTAACATTGAATTCAC 479				
464 CGCCTTACTGCTCGTGATTCATCCCGCAGTGGCGCGAGTCTATTAACATTGAATTCAC 523				
480 CCTCCCAAAACCTGTGGGCAATGATACCTGATGGGGAGCCTCTATTCAGGTGAGAT 539				
524 CCTCCCAAAACCTGTGGGCAATGATACCTGATGGGGAGCCTCTATTCAGGTGAGAT 583				
540 GATTAACACAGAGAGGTTATCAAGAGACTTAAAGGCTTTATGAAGACCAAAAGACAGTC 599				
584 GATTAACACAGAGAGGTTATCAAGAGACTTAAAGGCTTTATGAAGACCAAAAGACAGTC 643				
600 CTGNNATATTACAGAAAAAAGGGTGTGGAACATTCTCGGAACAAGAAACCAACAG 659				
644 CTGGAATATTACAGAAAAAAGGGTGTGGAACATTCTCGGAACAAGAAACCAACAG 703				
660 ATTGGCCATATGATATGCTTTCTTACAACTAAAGTTCCAAAGAACAGCAGAAAGCT 719				
704 ATTGGCCATATGATATGCTTTCTTACAACTAAAGTTCCAAAGAACAGCAGAAAGCT 763				

OY 720 TCAGTACTCATGAGAGAAATGTGTGTAATTAATAGTAAGGCAAACTCCT 779
|||||
DB 764 TCAGTACTCATGAGAGAAATGTGTGTAATTAATAGTAAGGCAAACTCCT 823
XX
OY 780 AGTCTTGATTTAGAAAGCTGCTTTTCTTAAGACTTCTAGTATGTAATGTAATCTTTGAAA 839
|||||
DB 824 AGTCTTGATTTAGAAAGCTGCTTTTCTTAAGACTTCTAGTATGTAATGTAATCTTTGAAA 883
OY 840 ATTATATTACTTTTA 854
|||||
DB 884 ATTATATTACTTTTA 898
|||||
RESULT 4
AAH14427
ID AAH14427 standard; cDNA: 2642 BP.
XX
AC AAH14427;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA sequence SEQ ID NO:11882.
XX
KM Human: primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN EPI074617-A2.
XX
PD 07-FEB-2001.
XX
PE 28-JUL-2000; 2000EP-0116126.
XX
PR 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-0300253.
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -
XX
XX
PS Claim 8: SEQ ID 11882; 2537bp + CD ROM; English.
XX
CC The present invention describes primer sets for synthesizing 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to

CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.

Sequence 2642 BP; 803 A; 503 C; 549 G; 787 T; 0 other;

Query Match 97.8%; Score 835.2; DB 22; Length 2642;

Best Local Similarity 99.2%; Pred. No. 4.4e-236;

Matches 848; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

OY 1 GCCAAGCCCAAGAGCCCTGTACCGCGCGGTG-0GGCCTAGTGTGGCCATGGGGCG 59
|||
DB 90 GCCAAGCCCAAGAGCCCTGTACCGCGCGGTG-0GGCCTAGTGTGGCCATGGGGCG 149
OY 60 TCCGCGCGGCTGCTGCGAGGGGTGATCATGGGGGCCCCGGGCTGGGCAAGGCAAGCTG 119
|||||
DB 150 TCCGCGCGGCTGCTGCGAGGGGTGATCATGGGGGCCCCGGGCTGGGCAAGGCAAGCTG 209
OY 120 TCGTCGGCATCACTACACTTGAAGTGAAGCAAGCTTGCACAGGGGACCTGCTCCGG 179
|||||
DB 210 TCGTCGGCATCACTACACTTGAAGTGAAGCAAGCTTGCACAGGGGACCTGCTCCGG 269
OY 180 GACAACATGCTGCGGGGACAGAAATTTGGCGTGTAAAGCAAGGCTTTTCAATTGACCAAGG 239
|||||
DB 270 GACAACATGCTGCGGGGACAGAAATTTGGCGTGTAAAGCAAGGCTTTTCAATTGACCAAGG 329
OY 240 AAACATCTCCCAAGATGATGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 299
|||||
DB 330 AAACATCTCCCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 389
OY 300 CAGTATAGCTGCGCTGTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 359
|||||
DB 390 CAGTATAGCTGCGCTGTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 449
OY 360 AGAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 419
|||||
DB 450 AGAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 509
OY 420 CGCCTTACTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 479
|||||
DB 510 CGCCTTACTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 569
OY 480 CTTCCCAAACTGTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 539
|||||
DB 570 CTTCCCAAACTGTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 629
OY 540 GATTAACACAGAGAGGCTTATCAAGAGACTTAAGGCTTATGAAGCAAAAGCAAGCAAGT 599
|||||
DB 630 GATTAACACAGAGAGGCTTATCAAGAGACTTAAGGCTTATGAAGCAAAAGCAAGCAAGT 689
OY 600 CTGGATATTTACAGAGAGAGGCTTATCAAGAGACTTAAGGCTTATGAAGCAAAAGCAAG 659
|||||
DB 690 CTGGATATTTACAGAGAGAGGCTTATCAAGAGACTTAAGGCTTATGAAGCAAAAGCAAG 749
OY 660 ATTGGGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 719
|||||
DB 750 ATTGGGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 809
OY 720 TCAGTACTCATGAGAGAAATGTGTGTAATTAATAGTAAGGCAAACTCCT 779
|||||
DB 810 TCAGTACTCATGAGAGAAATGTGTGTAATTAATAGTAAGGCAAACTCCT 869
OY 780 AGTCTTGATTTAGAAAGCTGCTTTTCTTAAGACTTCTAGTATGTAATGTAATCTTTGAAA 839
|||||
DB 870 AGTCTTGATTTAGAAAGCTGCTTTTCTTAAGACTTCTAGTATGTAATGTAATCTTTGAAA 929
OY 840 ATTATATTACTTTTA 854
|||||
DB 930 ATTATATTACTTTTA 944
RESULT 5
AAH33296

ID / AAH3296 standard; cDNA: 2765 BP.
XX
AC AAH3296;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen encoding cDNA SEQ ID NO:352.
XX
KW Human: colon cancer; colon cancer antigen; diagnosis; detection;
KW colorectal carcinoma; ss.
XX
OS Homo sapiens.
XX
PN WO200122920-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-US26524.
XX
PR 29-SEP-1999; 99US-0157137.
PR 03-NOV-1999; 99US-0163280.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
DR WPI: 2001-235357/24.
DR P-PSDB: AAG73865.
XX
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT useful for preventing, diagnosing and/or treating colorectal cancers -
XX
XX
PS Claim 1: Page 2462-2463; 9803pp; English.
XX
XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
XX cancer-associated nucleic acid molecules (N) and proteins (P), where
XX the proteins are collectively known as colon cancer antigens. The colon
XX cancer antigens have cytostatic activity and can be used in gene
XX therapy and vaccine production. N and P may be used in the prevention,
XX diagnosis and treatment of diseases associated with inappropriate P
XX expression. For example, N and P may be used to treat disorders
XX associated with decreased expression by rectifying mutations or deletions
XX in a patient's genome that affect the activity of P by expressing
XX inactive proteins or to supplement the patient's own production of P.
XX Additionally, N may be used to produce the colon cancer-associated Ps,
XX by inserting the nucleic acids into a host cell and culturing the cell
XX to express the proteins. N and P can be used in the prevention, diagnosis
XX and treatment of colorectal carcinomas and cancers. AAH37196 to
XX CC and AAG77789 represent sequences used in the exemplification of the
XX present invention.
XX CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
XX missing at time of publication, meaning no sequences are present for
XX CC SEQ ID NO:1027 to 1052, 7921 and 7922.
XX
SQ Sequence 2765 BP; 872 A; 523 C; 575 G; 793 T; 2 other:

Query Match 97.8%; Score 835.2; DB 22; Length 2765;
Best Local Similarity 99.2%; Pred. No. 4.5e-236;
Matches 848; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

DB 326 GACAAATGCTGGGGGACAGAAATTGGCGTGTAGCCAAAGCTTTCATTGACCAAGGG 385
|||||
QY 240 AAATCATCCAGATGATGTCATGACTGGGTGGCCCTTCATGAGCTGAAAATCTCACC 299
|||||
DB 386 AAATCATCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 445
|||||
QY 300 CAGTATAGCTGGCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 359
|||||
DB 446 CAGTATAGCTGGCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 505
|||||
QY 360 AGAGCTTATCAGATGACACAGATGATTAACCTGAATGTCCTTTCAGTATTAACAA 419
|||||
DB 506 AGAGCTTATCAGATGACACAGATGATTAACCTGAATGTCCTTTCAGTATTAACAA 565
|||||
QY 420 CGCTTACTGCTGCTGATTCATCCCGCAGTGGCCGAGTCTATTAATTAATTAAC 479
|||||
DB 566 CGCTTACTGCTGCTGATTCATCCCGCAGTGGCCGAGTCTATTAATTAATTAAC 625
|||||
QY 480 CCTCCCAAAAGTGGGCAATGATGACGTCGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 539
|||||
DB 626 CCTCCCAAAAGTGGGCAATGATGACGTCGACGAGGAGGAGGAGGAGGAGGAGGAGGAT 685
|||||
QY 540 GATTAACAGAGACGGTATCAAGAGACTTAAAGGCTTATGAAGACCAAAAGCAGTC 599
|||||
DB 686 GATTAACAGAGACGGTATCAAGAGACTTAAAGGCTTATGAAGACCAAAAGCAGTC 745
|||||
QY 600 CTGNNATATTACCAAAAAAGGGGTGCGAAGCAATTTCTCCGGAAACAAACCAAG 659
|||||
DB 746 CTGNNATATTACCAAAAAAGGGGTGCGAAGCAATTTCTCCGGAAACAAACCAAG 805
|||||
QY 660 ATTTGGCCCTATGATATGCTTCTCAACACTTAAAGTCCACAAAGAGCCAGAAAGCT 719
|||||
DB 806 ATTTGGCCCTATGATATGCTTCTCAACACTTAAAGTCCACAAAGAGCCAGAAAGCT 865
|||||
QY 720 TCAGTTACTTCATGAGGAAATGTGTGTAATTAATTAATTAATTAATTAATTAATTAATTA 779
|||||
DB 866 TCAGTTACTTCATGAGGAAATGTGTGTAATTAATTAATTAATTAATTAATTAATTAATTA 925
|||||
QY 780 AGCTCTGATTTAGAGAGCTGCTTTTCTTAAGACTCTGTGTAATTAATTAATTAATTAATTA 839
|||||
DB 926 AGCTCTGATTTAGAGAGCTGCTTTTCTTAAGACTCTGTGTAATTAATTAATTAATTAATTA 985
|||||
QY 840 ATTATATTACTTTTA 854
|||||
DB 986 ATTATATTACTTTTA 1000
|||||

RESULT 6
ABA09570
ID ABA09570 standard; cDNA: 2041 BP.
XX
AC ABA09570;
XX
DT 11-JAN-2002 (first entry)
XX
DE Human secreted protein homologue-encoding cDNA, SEQ ID NO:1346.
XX
XX
KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoietic regulation; tissue growth; immunomodulator; actlyin;
KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW antiasthmatic; antiarthritis; haemostatic; antiarteriosclerotic;
KW cytosstatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW antifungal; vulnery; antilucer; ss.
XX
OS Homo sapiens.


```

XX 26-DEC-2000; 2000MO-US34263.
PF
XX
PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0596042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao Q, Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI: 2001-442253/47.
DR P-PSDB: AAM40685.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX
PS Claim 1; SEQ ID NO 3830; 10078bp; English.
XX
XX The invention relates to human nucleic acids (AA157798-AA161369) and
XX the encoded polypeptides (AAM38642-AAM42213) with nootropic,
XX immunosuppressant and cyostatic activity. The polynucleotides are useful
XX in gene therapy. A composition containing a polypeptide or polynucleotide
XX of the invention may be used to treat diseases of the peripheral nervous
XX system, such as peripheral nervous injuries, peripheral neuropathy and
XX localised neuropathies and central nervous system diseases, such as
XX Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX utilisation of the activities such as: Immune system suppression,
XX Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX assays for receptor activity, arthritis and inflammation, leukaemias and
XX C.N.S disorders.
XX Note: The sequence data for this patent did not form part of the printed
XX specification.
XX
SQ Sequence 2432 BP; 771 A; 436 C; 489 G; 736 T; 0 other;

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Query Match          96.0%; Score 820; DB 22; Length 2432;
Best Local Similarity 99.8%; Pred. No. 1.3e-231;
Matches 820; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 33 GGGCTCACTCTGCGGCGCATGGGGGCGTCCGCGGCTGCTCGAGCGGTGATCATGGGG 92
   |||||||
DB 19 GGGCTCACTCTGCGGCGCATGGGGGCGTCCGCGGCTGCTCGAGCGGTGATCATGGGG 78
   |||||||
QY 93 GCGCGGGGCTCGGGGCGGCGACCGTGTGTCGGCGATCAGTACACACTTCGAGCTGAAG 152
   |||||||
DB 79 GCGCGGGGCTCGGGGCGGCGACCGTGTGTCGGCGATCAGTACACACTTCGAGCTGAAG 138
   |||||||
QY 153 CACCTCTCCAGGGGGGACCTGCTCGGGGACACATGCTCGGGGCGACCAAAATTTGGCGTG 212
   |||||||
DB 139 CACCTCTCCAGGGGGGACCTGCTCGGGGACACATGCTCGGGGCGACCAAAATTTGGCGTG 198
   |||||||
QY 213 TTAGCCAAAGCTTTTCAATTGACCAAGGAAACTATCCAGATGATGTCATGACTGGCTG 272
   |||||||
DB 199 TTAGCCAAAGCTTTTCAATTGACCAAGGAAACTATCCAGATGATGTCATGACTGGCTG 258
   |||||||
QY 273 GCGCTTCATGAGCTGAAAAATCTCAACCAGTATAGCTGCTGTGGATGTTTCCAAAG 332
   |||||||
DB 259 GCGCTTCATGAGCTGAAAAATCTCAACCAGTATAGCTGCTGTGGATGTTTCCAAAG 318
   |||||||
QY 333 ACACCTCCAGCAGCAAGACCCCTAGATAGAGCTTATCAGATGACACAGTATTAACCTG 392
   |||||||
DB 319 ACACCTCCAGCAGCAAGACCCCTAGATAGAGCTTATCAGATGACACAGTATTAACCTG 378
   |||||||

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QY 393 AATGTCCTCTTGAGCTCATTAACACACCCCTTACTGCTGCGTGATTCATCCGCGACT 452
   |||||||
DB 379 AATGTCCTCTTGAGCTCATTAACACACCCCTTACTGCTGCGTGATTCATCCGCGACT 438
   |||||||
QY 453 GCGCGAGTCTATTAACATTTCAATTCACCTCCCAAAACTGTGGGCAATTCATGACTGACT 512
   |||||||
DB 439 GCGCGAGTCTATTAACATTTCAATTCACCTCCCAAAACTGTGGGCAATTCATGACTGACT 498
   |||||||
QY 513 GGGGAGCCTCTGATGAGGTGAGTAAACCGAGACGCGTTTCAAGAGACTAAAG 572
   |||||||
DB 499 GGGGAGCCTCTGATGAGGTGAGTAAACCGAGACGCGTTTCAAGAGACTAAAG 558
   |||||||
QY 573 GCTTATGAAGACCAACCAAGCAGTCTCGNATATTTACAGAAAAAGGGGTGCGGAA 632
   |||||||
DB 559 GCTTATGAAGACCAACCAAGCAGTCTCGNATATTTACAGAAAAAGGGGTGCGGAA 618
   |||||||
QY 633 ACATTTCTCCGGAACAGAAACCAAGATTTGGCCCTATGATATGCTTTCTTCAAACT 692
   |||||||
DB 619 ACATTTCTCCGGAACAGAAACCAAGATTTGGCCCTATGATATGCTTTCTTCAAACT 678
   |||||||
QY 693 AAAGTCCCAACCAAGAAAGCAGAAAGCTTCAGTTACTCCAGGGAATGTTGTAAGT 752
   |||||||
DB 679 AAAGTCCCAACCAAGAAAGCAGAAAGCTTCAGTTACTCCAGGGAATGTTGTAAGT 738
   |||||||
QY 753 ATTAATAGTAAAGTGGGCAAACTCTCTAGCTCTGATTTAGAAAGCTCTTTTCTTAAGA 812
   |||||||
DB 739 ATTAATAGTAAAGTGGGCAAACTCTCTAGCTCTGATTTAGAAAGCTCTTTTCTTAAGA 798
   |||||||
QY 813 CTCTAGTATGATGATTAATCTTTGAAAATTAATTAATTTACTTTTA 854
   |||||||
DB 799 CTCTAGTATGATGATTAATCTTTGAAAATTAATTAATTTACTTTTA 840
   |||||||
RESULT 8
AA158055
ID AA158055 standard; cDNA; 2421 BP.
XX
XX AA158055;
AC
XX
XX 22-OCT-2001 (first entry)
DT
XX
XX Human polynucleotide SEQ ID NO 258.
DE
XX
XX Human; nootropic; immunosuppressant; cyostatic; gene therapy; cancer;
XX peripheral nervous system; neuropathy; central nervous system; CNS;
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
XX chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
XX leukaemia; ss.
XX
XX Homo sapiens.
XX
XX WO200153312-A1.
XX
XX 26-JUL-2001.
XX
XX 26-DEC-2000; 2000MO-US34263.
PF
XX
XX 21-JAN-2000; 2000US-0488725.
XX
XX 25-APR-2000; 2000US-0552317.
XX
XX 09-JUL-2000; 2000US-0596042.
XX
XX 19-JUL-2000; 2000US-0620312.
XX
XX 03-AUG-2000; 2000US-0653450.
XX
XX 14-SEP-2000; 2000US-0662191.
XX
XX 19-OCT-2000; 2000US-0693036.
XX
XX 29-NOV-2000; 2000US-0727344.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
XX Zhao Q, Zhou P, Goodrich R, Drmanac RT;
XX

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CC AAH13633 to AAH18742 represent human cDNA sequences: AAB92446 to
 CC AAB95893 represent human amino acid sequences; and AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.

SO Sequence 2394 BP; 760 A; 428 C; 477 G; 729 T; 0 other;

Query Match 95.6%; Score 816; DB 22; Length 2394;
 Best Local Similarity 99.8%; Pred. No. 2e-230;
 Matches 816; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 37 CTCAGCTCTGCGCCATGCGGGCGTCCGCGCGCTGCTGCGAGCGGTGATCATGGGGCCC 96
 DB 1 CTCAGCTCTGCGCCATGCGGGCGTCCGCGCGCTGCTGCGAGCGGTGATCATGGGGCCC 60
 QY 97 CGGGGTCGGGCAAGGCGACCGTGTGCGGCATCATCTACACATTCGAGCGAAGCACCC 156
 DB 61 CGGGGTCGGGCAAGGCGACCGTGTGCGGCATCATCTACACATTCGAGCGAAGCACCC 120
 QY 157 TCTCCAGCGGGGACCTGCTCCGGGCAACATGCTGCGGGGACAGAAATTTGGCGTTAG 216
 DB 121 TCTCCAGCGGGGACCTGCTCCGGGCAACATGCTGCGGGGACAGAAATTTGGCGTTAG 180
 QY 217 CCAAGGCTTTCATTGACCAAGGGAATCTATCCAGATGATGTCACTCGGCTGGCCC 276
 DB 181 CCAAGGCTTTCATTGACCAAGGGAATCTATCCAGATGATGTCACTCGGCTGGCCC 240
 QY 277 TTCATGAGCTGAAAATATCCACAGTATAGTGGTGTGATGTTTCCAAAGGACAC 336
 DB 241 TTCATGAGCTGAAAATATCCACAGTATAGTGGTGTGATGTTTCCAAAGGACAC 300
 QY 337 TTCACAGGCGACAGCCCTAGATAGAGCTTATCAGATCGACAGTGTATTAACCTGAATG 396
 DB 301 TTCACAGGCGACAGCCCTAGATAGAGCTTATCAGATCGACAGTGTATTAACCTGAATG 360
 QY 397 TCCCTTTGAGTCTATTAAACAGCGCTTACTGCTGCTGATTCATCCCGCAGTGGCC 456
 DB 361 TCCCTTTGAGTCTATTAAACAGCGCTTACTGCTGCTGATTCATCCCGCAGTGGCC 420
 QY 457 GAGTATTAACATTAATTCACACCCCTCCCAAAAGTGGGCGTATGATGCTGAGTGGGG 516
 DB 421 GAGTATTAACATTAATTCACACCCCTCCCAAAAGTGGGCGTATGATGCTGAGTGGGG 480
 QY 517 AGCCTCTCATTCAGCGGTGAGATGATTAACAGAGACGGTTATCAAGAGACTAAAGGCTT 576
 DB 481 AGCCTCTCATTCAGCGGTGAGATGATTAACAGAGACGGTTATCAAGAGACTAAAGGCTT 540
 QY 577 ATGAAGACCAACAAGNCAGTCTGCGNATTTACACAAAAAGGGGTCTGGAACAT 636
 DB 541 ATGAAGACCAACAAGNCAGTCTGCGNATTTACACAAAAAGGGGTCTGGAACAT 600
 QY 637 TCTCGGAACAGAAACCAAGATTTGGCCCTATGTATATGCTTCCACAAACTAAG 696
 DB 601 TCTCGGAACAGAAACCAAGATTTGGCCCTATGTATATGCTTCCACAAACTAAG 660
 QY 697 TTCCACAAGAAGCCAGAAGCTTCACTACTCATGAGAGAAATGTGTACTATTA 756
 DB 661 TTCCACAAGAAGCCAGAAGCTTCACTACTCATGAGAGAAATGTGTACTATTA 720
 QY 757 ATAGTAAGATGGGCAAACTCTAGTCTTGCATTTAGAGCTGCTTTCTTAAGACTTC 816
 DB 721 ATAGTAAGATGGGCAAACTCTAGTCTTGCATTTAGAGCTGCTTTCTTAAGACTTC 780
 QY 817 TAGTATGATGAATCTTTGAATAATTAATTAATCTTTA 854
 DB 781 TAGTATGATGAATCTTTGAATAATTAATTAATCTTTA 818

RESULT 10
 AAH47197
 ID AAH47197 standard; CDNA: 2394 BP.
 XX
 AC AAH47197;

XX 30-NOV-2001 (first entry)
 DR
 XX
 DE Human adenylate kinase 3 (AK3)-like protein encoding cDNA.

KW Adenylate kinase 3-like protein; AK3-like protein; AK3; cell morphology;
 KW MELAS; central nervous system disorder; epilepsy; skeletal muscle;
 KW muscle disease; electron transfer disorder; leber disease; human;
 KW diabetes mellitus; Pearson disease; Parkinson's disease;
 KW metabolism disorder; ss.

OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS 15..698

FT /tag= a

FT /product= "AK3-like protein"

PN WO200109346-A1.

PD 08-FEB-2001.

PP 28-JUL-2000; 2000WO-JP05066.

PR 29-JUL-1999; 99JP-0248036.

PR 27-AUG-1999; 99JP-0300253.

PR 18-OCT-1999; 99US-0159590.

PR 11-JAN-2000; 2000JP-0118776.

PR 17-FEB-2000; 2000US-0183322.

XX (HELI-) HELIX RES INST.

PI Ota T, Isogai T, Hayashi K, Saito K, Yamamoto J, Ishii S;
 PI Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Ihara S, Nakae H;
 PI Nishikawa T, Kimura K;

DR WPI: 2001-564737/63.

DR P-PSDB: AAB85885.

PT New gene encoding an adenylate kinase 3-like protein, and the protein
 PT and antibodies to it, useful for diagnosis of brain disease e.g.
 PT epilepsy, muscle disease, genetic disorder, diabetes

PS Claim 1; Page 32-34; 41pp; Japanese.

CC The invention relates to a cDNA (clone C-NT2RP2000329) encoding a novel
 CC adenylate kinase 3 (AK3)-like protein. C-NT2RP2000329 has functions of
 CC converting extracellular signals into intracellular signals and changing
 CC cell morphology. The AK3-like protein, polynucleotides and antibodies are
 CC useful in the investigation of diseases such as MELAS (cerebral accident
 CC condition with hyperlactacidemia), central nervous system disorder,
 CC epilepsy, skeletal muscle conditions, muscle disease, electron transfer
 CC disorders, leber disease, diabetes mellitus, Pearson disease, Parkinson's
 CC disease, metabolism disorders. They are useful for developing diagnostics
 CC and treatment agents. The present sequence represents a cDNA encoding a
 CC human AK3-like protein of the invention.

SO Sequence 2394 BP; 760 A; 428 C; 477 G; 729 T; 0 other;

Query Match 95.6%; Score 816; DB 22; Length 2394;
 Best Local Similarity 99.8%; Pred. No. 2e-230;
 Matches 816; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 37 CTCAGCTCTGCGCCATGCGGGCGTCCGCGCGCTGCTGCGAGCGGTGATCATGGGGCCC 96
 DB 1 CTCAGCTCTGCGCCATGCGGGCGTCCGCGCGCTGCTGCGAGCGGTGATCATGGGGCCC 60
 QY 97 CGGGCTCGGCAAGGCGACCGTGTGCGGCATCATACACACTTCGAGCTGAAGCACCC 156
 DB 61 CGGGCTCGGCAAGGCGACCGTGTGCGGCATCATACACACTTCGAGCTGAAGCACCC 120
 QY 157 TCTCCAGCGGGGACCTGCTCCGGGCAACATGCTGCGGGGACAGAAATTTGGCGTTAG 216

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Db 121 TCTCAGCGGGGACCTGCTCCGGGACAACATGCTGCGGGGACAGAAATTGGCGTTAG 180
QY 217 CCAAGGCTTTCATTGACCAAGGGAATCTCATCCAGATGATGTATACTCGGCTGGCCC 276
Db 181 CCAAGGCTTTCATTGACCAAGGGAATCTCATCCAGATGATGTATACTCGGCTGGCCC 240
QY 277 TTCATAGCTGAAAAATCTCACCAGTATAGCTGGCTGGTGGATGTTTCCAGAGCAC 336
Db 241 TTCATAGCTGAAAAATCTCACCAGTATAGCTGGCTGGTGGATGTTTCCAGAGCAC 300
QY 337 TTCACAGCGAGAACCCCTAGATAGACCTTATCAGATGCACACAGTAACTGAATG 396
Db 301 TTCACAGCGAGAACCCCTAGATAGACCTTATCAGATGCACACAGTAACTGAATG 360
QY 397 TGGCCTTTGAGCTATTAACAAGCGCTTACTGCTCGCTGATTCATCCCGCAGTGCC 456
Db 361 TGGCCTTTGAGCTATTAACAAGCGCTTACTGCTCGCTGATTCATCCCGCAGTGCC 420
QY 457 GAGCTATTAACATTTGAATTCACCCCTCCAAAACCTGGGCATTTGATGACCTGACGGG 516
Db 421 GAGCTATTAACATTTGAATTCACCCCTCCAAAACCTGGGCATTTGATGACCTGACGGG 480
QY 517 AGCCTCATTTACGCGTGAAGATGATTAACACAGAGCGTTATCAAGACTAAAGCCTT 576
Db 481 AGCCTCATTTACGCGTGAAGATGATTAACACAGAGCGTTATCAAGACTAAAGCCTT 540
QY 577 ATGAGACCAACAAAGNCAGTCTGATATTACCAAAAAAGGGGCTGTGAAACAT 636
Db 541 ATGAGACCAACAAAGNCAGTCTGATATTACCAAAAAAGGGGCTGTGAAACAT 600
QY 637 TCTCCGAGACAAACCAACAGATTTGGCCCTATGATATGCTTCTTACAACTAAG 696
Db 601 TCTCCGAGACAAACCAACAGATTTGGCCCTATGATATGCTTCTTACAACTAAG 660
QY 697 TTCCACAAAAGCGCAGAAAGCTTCACTTACTCATGAGGAAATGTGTAACTATTA 756
Db 661 TTCCACAAAAGCGCAGAAAGCTTCACTTACTCATGAGGAAATGTGTAACTATTA 720
QY 757 ATAGTAGATGAGCAACCTCTAGTCTTGTGATTTAGAACTGCTTCTTCTAAGACTTC 816
Db 721 ATAGTAGATGAGCAACCTCTAGTCTTGTGATTTAGAACTGCTTCTTCTAAGACTTC 780
QY 817 TAGTAGTAGAATTTCTTGAATAATTAATTACTTTTA 854
Db 781 TAGTAGTAGAATTTCTTGAATAATTAATTACTTTTA 818

RESULT 11
AAA60582
ID AAA60582 standard; cDNA; 751 BP.
XX
AC AAA60582:
XX
DT 20-OCT-2000 (first entry)
XX
DE Human mitochondrial GTP:AMP phosphotransferase encoding cDNA SEQ ID NO:3.
KM Human: mitochondrial GTP:AMP phosphotransferase; GTP3P; ribotide; ss.
XX
OS Homo sapiens.
XX
PN CN1249340-A.
XX
PD 05-APR-2000.
XX
PF 28-SEP-1998; 98CN-0119439.
XX
PR 28-SEP-1998; 98CN-0119439.
XX
PA (XINH-) XINHUANGPU FUDAN GENE ENG CO LTD SHANGHA.
XX
PI Yu L, Zhao Y, Bi A;
XX
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DR WPI: 2000-400718/35.
DR P-PSDB; AAB12440.
XX
PT Preparation of human mitochondrial matrix GTP : AMP phosphotransferase,
PT its encode sequence -
XX
PS Claim 1; Page 14; 20pp; Chinese.
XX
CC The present invention describes a new ribotide sequence of human gene,
CC that is, the cDNA sequence of human mitochondrial matrix GTP:AMP
CC phosphotransferase (GTP3P) and the encoded polypeptide. The present
CC sequence encodes human GTP3P.
XX
SQ Sequence 751 BP; 211 A; 189 C; 186 G; 165 T; 0 other:

Query Match 85.5%; Score 729.8; DB 21; Length 751;
Best Local Similarity 98.1%; Pred. No. 3,2e-205;
Matches 737; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 51 ATGGGGGCGTCCGGCGGCTGCTGAGCGGTGATCATGGGGCCCGGCTCGGGCAG 110
Db 1 ATGGGGCGGCGCGGCGGCTGCTGAGCGGTGATCATGGGGCCCGGCTCGGGCAG 60
QY 111 GGCACCGTTCGTCGCGCATCTACACACTTCGAGCTGAAGACACTCTCCAGCGGGAC 170
Db 61 GGCACCGTTCGTCGCGCATCTACACACTTCGAGCTGAAGACACTCTCCAGCGGGAC 120
QY 171 CTGCTCCGGGACAAACATGCTCGGGGCGACAGAAATTTGGCGTTTACCAAGCTTTTCA 230
Db 121 CTGCTCCGGGACAAACATGCTCGGGGCGACAGAAATTTGGCGTTTACCAAGCTTTTCA 180
QY 231 GACCAAGGAAACATCCGCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 290
Db 181 GACCAAGGAAACATCCGCCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
QY 291 AATCTCACCGATATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 350
Db 241 AATCTCACCGATATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 351 GCCCTAGTAGAGCTTATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 410
Db 301 GCCCTAGTAGAGCTTATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
QY 411 ATTAACAACAGCCCTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 470
Db 361 ATTAACAACAGCCCTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 471 GAATTTCAACCTCTCCAAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 530
Db 421 GAATTTCAACCTCTCCAAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 531 CGTAGAGATGATTAACAGAGACGCTTATCAAGAGACTTAAGGCTTATGAAGACCAACA 590
Db 481 CGTAGAGATGATTAACAGAGACGCTTATCAAGAGACTTAAGGCTTATGAAGACCAACA 540
QY 591 AAGNCAGTCTGAGNATATTACAGAAAAAAGGGGTGCTGGAACATTTCCGGGACAGAA 650
Db 541 AAGNCAGTCTGAGNATATTACAGAAAAAAGGGGTGCTGGAACATTTCCGGGACAGAA 600
QY 651 ACCAACAAGATTTGGCCCTATGATATGCTTCTTACAACTAAAGTTCCACAAAGAGC 710
Db 601 ACCAACAAGATTTGGCCCTATGATATGCTTCTTCCACAACTAAAGTTCCACAAAGAGC 660
QY 711 CAGAAAGCTTAGTTACTCCATGAGGAGAAATGTGTACTATTAATAGTAAGTGGC 770
Db 661 CAGAAAGCTTAGTTACTCCATGAGGAGAAATGTGTACTATTAATAGTAAGTGGC 720
QY 771 AAACCTCTAGTCTTGCATTTAGAGCTGC 801
Db 721 AAACCTCTAGTCTTGCATTTAGAGCTGC 751

RESULT 12
```

AAC98376 standard; cDNA; 733 BP.
ID AAC98376 standard; cDNA; 733 BP.
XX AAC98376;
AC AAC98376;
XX
DT 09-MAR-2001 (first entry)
XX
DE Human colon cancer antigen nucleotide sequence SEQ ID NO:386.
XX
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW identification; cytostatic; cardioactive; neuroprotective; vulnery;
KW immunomodulatory; muscular; gynaecological; gastrointestinal;
KW nephrotropic; antiinfective; antibacterial; gene therapy; wound;
KW neural disorder; immune system disorder; muscular disorder;
KW reproductive disorder; gastrointestinal disorder; renal disorder;
KW infectious disease; cardiovascular disorder; ss.
XX
OS Homo sapiens.
XX
PN WO20005351-A1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000MO-US05883.
XX
PR 12-MAR-1999; 99US-0124270.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
PI WPI; 2000-587534/55.
XX
PI P-PSDB; AAB53619.
XX
DR
XX
PT Colon cancer associated gene sequences, referred to as colon cancer
PT antigens, useful for the treatment, prevention, and diagnosis of colon
PT disorders such as colon cancer -
XX
XX Claim 1; Page 849; 2104pp: English.
XX
XX AAC97991 to AAC98763 encode the human colon cancer associated proteins,
XX called human colon cancer antigens, given in AAB53234 to AAB54006. The
XX human colon cancer antigens can have cytosolic, cardioactive, muscular;
XX neuroprotective, immunomodulatory, gynaecological, gastrointestinal,
XX vulnerarly, nephrotropic, antiinfective and antibacterial activities, and
XX can be used in gene therapy. The colon cancer antigen polynucleotides,
XX proteins and antibodies to the proteins are useful for the prevention,
XX treatment and diagnosis of colon disorders, such as colon cancer. The
XX polynucleotides may be used in diagnostics and research, such as for
XX chromosome identification, and as hybridisation probes. The proteins
XX may also be used to prevent diseases such as neural disorders, immune
XX system disorders, muscular disorders, reproductive disorders,
XX gastrointestinal disorders, wounds, renal disorders, infectious
XX diseases, and cardiovascular disorders. AAC98764 to AAC98772 and
XX AAB54007 represent sequences used in the exemplification of the present
XX invention.
XX
XX Sequence 733 BP; 213 A; 175 C; 173 G; 168 T; 4 other;
XX
Query Match 81.0%; Score 691.4; DB 21; Length 733;
Best Local Similarity 97.5%; Pred. No. 7e-194;
Matches 709; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

Db 121 ACAGAAATTGGCGTTAGACCAAGGCTTTCATTGACCAAGGAAATCATCCAGATGAT 180
Qy 258 GTCATGACGCGCTGCGCCCTTCATGAGCTGAAAATCTCACCCAGTATGAGCTGGTGG 317
Db 181 GTCATGACGCGCTGCGCCCTTCATGAGCTGAAAATCTCACCCAGTATGAGCTGGTGG 240
Qy 318 GATGTTTTCCAAAGACACTTCCACAGGCAAGCCCTAGTAGCTTATCAGATGAC 377
Db 241 GATGTTTTCCAAAGACACTTCCACAGGCAAGCCCTAGTAGCTTATCAGATGAC 300
Qy 378 ACAATGATTAACCTGAATGTGCCCTTTGAGAGCTATTAAACAGCCCTTACTGCTGG 437
Db 301 ACAATGATTAACCTGAATGTGCCCTTTGAGAGCTATTAAACAGCCCTTACTGCTGG 360
Qy 438 ATTATCCCGCAGTGGCCGAGTCTATATACATTGAATTCACCCCTCCAAACGTGGGG 497
Db 361 ATTATCCCGCAGTGGCCGAGTCTATATACATTGAATTCACCCCTCCAAACGTGGGG 420
Qy 498 ATTATGACCTGACTGGGAGCCCTCTCATTCAGCGTAGGATGATTAACAGAGACGGT 557
Db 421 ATTATGACCTGACTGGGAGCCCTCTCATTCAGCGTAGGATGATTAACAGAGACGGT 480
Qy 558 ATCAAGAGACTAAAGGCTTTGAAGACCAACAGACAGTCTGATTTACAGAAA 617
Db 481 ATCAAGAGACTAAAGGCTTTGAAGACCAACAGACAGTCTGATTTACAGAAA 540
Qy 618 AAAGGGGTGCTGGAACATTCCTCGGAAACCAAGAAAGATTTGGCCCTATGATAT 677
Db 541 AAAGGGGTGCTGGAACATTCCTCGGAAACCAAGAAAGATTTGGCCCTATGATAT 600
Qy 678 GCTTTCCTACAAACTAAAGTTCCACAAAGACAGAAAGCTTCACTGATCAGTAGAGA 737
Db 601 GCTTTCCTACAAACTAAAGTTCCACAAAGACAGAAAGCTTCACTGATCAGTAGAGA 659
Qy 738 GAATGTGTACTATATATAGATGCGCAACCTCTGATGCTTCAATTTAGAAAG 797
Db 660 GAATGTGTACTATATATAGATGCGCAACCTCTGATGCTTCAATTTAGAAAG 719
Qy 798 CTGCTTT 804
Db 720 TGGTTTT 726
RESULT 13
AAH06376
ID AAH06376 standard; cDNA; 851 BP.
XX
AC AAH06376;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA clone (5'-primer) SEQ ID NO:3211.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-0116126.
XX
PR 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-0300253.
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX WPI; 2001-318749/34.
DR

PT Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -

PS Claim 1; SEQ ID 3211; 2537pp + CD ROM; English.

CC The present invention describes primer sets for synthesizing 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesizing polynucleotides
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialized methods. AAH03166 to AAH13658 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.

Sequence 851 BP; 215 A; 224 C; 233 G; 176 T; 3 other;

Query Match	77.2%	Score 659.2;	DB 22;	Length 851;
Best Local Similarity	94.8%	Pred. No. 2.5e-184;		
Matches 723; Conservative	0;	Mismatches 33;	Indels 7;	Gaps 4

QY	1	GCCANAGCCAAAGGCGCTGGTACCAGCGCGGGT-GGGCTCAGTGTGGGGCATGGGGGG	59
Db	90	GCGCAGGCGCAAAAGCCCTGGTACCAGCGCGGGT-CAGTGTGGGGCATGGGGGG	149
QY	60	TCCGCGGGGCTGTCGAGGCGGTATCATGGGGGCCCGGGGCTTCGGGCAAGGGGCAAGCTG	119
Db	150	TCCGCGGGGCTGTCGAGGCGGTATCATGGGGGCCCGGGGCTTCGGGCAAGGGGCAAGCTG	209
QY	120	TCTGTGGGCATCACTACACACTTCGAGCTGAGCACCCTTCACAGGGGAGCTGCTCGG	179
Db	210	TCTGTGGGCATCACTACACACTTCGAGCTGAGCACCCTTCACAGGGGAGCTGCTCGG	269
QY	180	GACAACTATGCGCGGGGCGACGAAATTTGGGGTGTATACCAAGGCTTCATTGAGCCAAAGG	239
Db	270	GACAACTATGCGCGGGGCGACGAAATTTGGGGTGTATACCAAGGCTTCATTGAGCCAAAGG	329
QY	240	AAACTATCCAGATGATGTATCATCTACCTCGGCTGGCCCTTATGAGTGGAAAAATCTAC	299
Db	330	AAACTATCCAGATGATGTATCATCTACCTCGGCTGGCCCTTATGAGTGGAAAAATCTAC	389
QY	300	CAGTATAGCTGGCTGTGGATGGTTTCCAAAGCAGCACTTCACAGGCGAGAAAGCCCTAGAT	359
Db	390	CAGTATAGCTGGCTGTGGATGGTTTCCAAAGCAGCACTTCACAGGCGAGAAAGCCCTAGAT	449
QY	360	AGAGCTTATAGATCGACACAGTATTAACCTGAAATGGCCCTTGGAGTCATTAACAA	419
Db	450	AGAGCTTATAGATCGACACAGTATTAACCTGAAATGGCCCTTGGAGTCATTAACAA	509
QY	420	CGCCTTACTGCTCGCTGGATTCATCCCGCAGTGGCCGAGTCTATAATGGAATTAAC	479
Db	510	CGCCTTACTGCTCGCTGGATTCATCCCGCAGTGGCCGAGTCTATAATGGAATTAAC	569
QY	480	CTTCCCAAAACTGTGGCATTTGATGACCTGACTGGGAGCCTTCATTCAAGCTGAGAT	539

Accession	Sequence	Position
D8	CTCTCCCAAACTGTGGGCGATTGATGACCTGACTGGGGAGCCTCTCATTTCACTGAGCGAT	6238
QY	540 GATAAACACGAGACGGTTATCAGAGACTAAAGCCTTATGAGACCAACAAACGACATC	599
D8	630 GATAAACACGAGACGGTTATCAGAGACTAAAGCCTTATGAGACCAACAAACGACATC	688
QY	600 CTGGAATTTTACCGAAAAAGGGGTCTGGAACATTTCGCCGACAGAAACCAACAAAG	655
D8	690 CTGGAATTTTACCGAAAAAGGGGTCTGGAACATTTCGCG-ACGAAACCAACAAAG	748
QY	660 ATTTGGCCCTATGTATATGCTTTCTACAAACTAAAGTTTCCACAAAGACGACAAAGCT	719
D8	749 ATTTGG-CCATGNNATATGCTTTCTACAAACTAAAGTTTCCACAAAGAACGCCAAGCT	807
QY	720 TCAGTTACTCCATGAGG----AAATGTGTATCAATTAAT	758
D8	808 TTAACTTACTTCCATGAAGAGGAAATGTGTGTAACCTTTAAT	850

RESULT 14

ID AAH05788 standard; cDNA; 639 BP

AC AAH05788;

DT 26-JUN-2001 (first entry)

DE Human cDNA clone (5'-primer) SEQ ID NO:2623.

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

OS Homo sapiens

PN EP1074617-A2

PD 07-FEB-2001

PF 28-JUL-2000; 2000EP-0116126.

PR 29-JUL-1999; 99JP-0248036.

PR 11-JAN-2000; 2000JP-0118776.

PR 09-JUN-2000; 2000JP-0241899.

PA (HELI-) HELIX RES INST.

PI Ota T, Isogai T, Nishikawa

XX

XX

PT full-length cDNAs defined in the specification, and for

PT full-length cDNAs -

PS Claim 1; SEQ ID 2623; 2537pp + CD ROM; English.

CC The present invention describes primer sets for synthesising 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesising polynucleotides


```
Db 302 AAACATCATCCAGATGATGTCATGACACGCGCTGCGCCCTTCATGAGCTGAAAAATCTCACC 361
QY 300 CAGTATAGCTGGCTGTTGGATGGTTTCCAGACACTTCCACAGGACAGAAAGCCCTAGAT 359
Db 362 CAGTATAGCTGGCTGTTGGATGGTTTCCAGACACTTCCACAGGACAGAAAGCCCTAGAT 421
QY 360 AGAGCTTATCGATCGACACAGATTAACCTGAATGCGCCTTGAGTCAATTAAACAA 419
Db 422 AGAGCTTATCGATCGACACAGATTAACCTGAATGCGCCTTGAGTCAATTAAACAA 481
QY 420 CGCCTTACTGCTGCTGATTCATCCGCGCAGTGGCCGAGTCTATAACATTGAATTCAAC 479
Db 482 CGCCTTACTGCTGCTGATTCATCCGCGCAGTGGCCGAGTCTATAACATTGAATTCAAC 541
QY 480 CCTCCCAAAACTGTGGCATTGATGACCTGACTGGGGAGGCTCTCATTC-AGCGTGAGA 538
Db 542 CCTCCCAAAACTGTGGCATTGATGACCTGACTGGGGAGGCTCTCATTCAGCGTGAGA 601
QY 539 -TGATAACCGAGAGCGTATCAAGAGACTAAAGCTTATGAAGCAACAAAGNCAG 597
Db 602 TTGATAAACGAGACGCTTATCAAGAGACTAAAGGCTTATGAAGCAACAAAGCCAG 661
QY 598 TCCTGNAFTATTACGAAAAAAGGGTGCTG 629
Db 662 TCCTGGATATTACCAAGAAAAAAGGGGTG 693
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Search completed: March 19, 2003, 04:26:18
Job time : 264 secs

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OM nucleic - nucleic search, using sw model

Run on: March 19, 2003, 03:11:20 ; Search time 1475 Seconds
(without alignments)
9376.912 Million cell updates/sec

Title: US-10-006-190-2

Perfect score: 854
Sequence: 1 GCCAGCCCAAGAGCCCTGGT.....TGAAATATATTACTTTTA 854

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 809774376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estlinu:*
5: em_estlov:*
6: em_estlpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hic:*
12: gb_estl3:*
13: gb_estl4:*
14: gb_estl5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	832.6	97.5	1070	14	BM923355
2	797.4	93.4	979	14	BQ650443
3	699.2	81.9	1024	14	BQ050240
4	684.6	80.2	795	13	B1550730
5	659.2	77.2	706	12	BG705248
6	659.2	77.2	851	9	AU130170

7	637.2	74.6	716	10	AV704895	AV704895
8	635.4	74.4	1183	12	BG106150	BG106150
9	633.8	74.2	924	14	BQ435142	BQ435142
10	623.8	73.3	833	13	B1553812	B1553812
11	605	70.8	902	12	BG619950	BG619950
12	595.2	69.7	639	9	AU126983	AU126983
13	594.2	69.6	716	10	AV695155	AV695155
14	581	68.0	711	12	BG687423	BG687423
15	578.6	67.8	803	9	AU136907	AU136907
16	573.4	67.1	1095	11	AK008681	AK008681
17	571.8	67.0	2758	11	AK004864	AK004864
18	571.8	67.0	2805	11	AK005194	AK005194
19	564.6	66.1	616	10	AV698046	AV698046
20	560.2	65.6	723	12	BG682861	BG682861
21	559	65.5	743	9	AL138385	AL138385
22	557.6	65.3	907	14	BQ714961	BQ714961
23	543	63.6	789	13	B1601992	B1601992
24	533.4	62.5	1110	13	B1415807	B1415807
25	529.2	62.0	616	10	AV707926	AV707926
26	528.4	61.9	705	12	BG698420	BG698420
27	526.2	61.6	870	13	B1257720	B1257720
28	523.6	61.3	626	14	BQ367213	BQ367213
29	511.4	59.9	802	13	B1601245	B1601245
30	508.2	59.5	1286	12	BG115825	BG115825
31	506.6	59.3	815	13	B1328500	B1328500
32	494.4	57.9	496	12	BF514669	BF514669
33	491.8	57.6	495	12	BF513711	BF513711
34	490	57.4	525	14	BQ270849	BQ270849
35	489.8	57.4	643	13	B8621249	B8621249
36	484.4	56.7	918	13	B1858992	B1858992
37	483	56.6	917	11	AK007618	AK007618
38	482.8	56.5	650	9	AI119333	AI119333
39	476.4	55.8	636	10	BB656931	BB656931
40	474.8	55.6	515	9	AA007279	AA007279
41	471.8	55.2	1137	13	BM478239	BM478239
42	471.2	55.2	522	13	BM272857	BM272857
43	471.2	55.2	600	14	BM637013	BM637013
44	469.6	55.0	700	13	B1561819	B1561819
45	465	54.4	677	14	BQ694111	BQ694111

ALIGNMENTS

RESULT 1
LOCUS BM923355 1070 bp mRNA linear EST 12-MAR-2002
DEFINITION AGENCOURT_6625937 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5758957
5', mRNA sequence.

ACCESSION BM923355
VERSION BM923355.1 GI:19373734
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1070)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA sequencing by: Agencourt Bioscience Corporation
Cloned through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: L1AM12803 row: j column: 14
High quality sequence stop: 686.
Location/Qualifiers 1. 1070

FEATURES
source

QY	827	GAATCTTTGA	840
	1		
Db	780	GGATTCTTGAAA	793

RESULT 4	BI550730	795 bp	mRNA	linear	EST 05-SEP-2001
LOCUS	BI550730				
DEFINITION	60319561P1 NIH_MGC_95 Homo sapiens		CDNA	clone IMAGE:5274916 5'	
ACCESSION	BI550730				
VERSION	BI550730.1	GI:15438042			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
AUTHORS	1 (bases 1 to 795)				
TITLE	NIH-MGC http://mgc.nci.nih.gov/.				
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: M.I.K.O.S. Palkovits, M.D., Ph.D. CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiroki Toshiyuki and Piero Carninci (RIKEN) CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.gov Plate: L16M1694 row: b column: 05 High quality sequence stop: 763.				

FEATURES	source
location/Qualifiers	1..795
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="IMAGE:5274916"	
/clone_lib="NIH_MGC_95"	
/tissue_type="hippocampus"	
/lab_host="DH10B"	
/note="Organ: brain; Vector: pBluescript (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag) ; Oligo-dT primed using primer 5'-TTTTTGTGTTT-3' size-selected for average insert size 2.5 kb and normalized to R0F 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."	

BASE COUNT	207 a	208 c	220 g	160 t
ORIGIN				
Query Match	80.2%	Score 684.6;	DB 13;	Length 795;
Best Local Similarity	97.8%	Pred. No. 1e-183;		
Matches 745;	Conservative	0;	Mismatches 12;	Indels 5;
			Gaps	5;

QY	1	GCCANGCCCAAGCCCTGTACCGCGCGGGG-GGGCTCAGTGTGCGGCCCATGGGGCG	59
Db	23	GGCCAGGCCCAAGCCCTGTGTACCGCGGGGCGGCTCAGTGTGCGGCCCATGGGGCG	82
QY	60	TCCGCGCGGCTGTCTGCGAGCGGTATCATGTGGGGGCCCGGCGTGGCGCAAGGCGACGCTG	119
Db	83	TCCGCGCGGCTGTCTGCGAGCGGTATCATGTGGGGGCCCGGCGTGGCGCAAGGCGACGCTG	142
QY	120	TCTGTGCGGCATACATACACACTTGCAGCTGAAGCACCTCTCCAGCGGGGACCTGCTCCGG	179
Db	143	TCTGTGCGGCATACATACACACTTGCAGCTGAAGCACCTCTCCAGCGGGGACCTGCTCCGG	202
QY	180	GACAAATGCTGGGGGGGACAGAAATTGGCGCTTTAGCAAGCGTTTATTGACCAAGG	239
Db	203	GACAAATGCTGGGGGGGACAGAAATTTGGCGCTTTAGCAAGCGTTTATTGACCAAGG	262

Oy	240	AAATCATTCCAGATGATGTCATGCCTCGGGGCCCTTCAATGACCTGAATAAATCTCAC	299
Db	263	AAATCATCCAGATGATGTCATGCCTCGGGGCCCTTCAATGACCTGAATAAATCTCAC	322
Oy	300	CAGATAGCTGGCTGTGGATGTTTTCCAAGGACACTTCCACAGCAGAACCCTAGAT	359
Db	323	CAGATAGCTGGCTGTGGATGTTTTCCAAGGACACTTCCACAGCAGAACCCTAGAT	382
Oy	360	AGACTTATCGATTCGACACAGTAGTTAACTGATGTGCCCTTGAGTCAATTAAACA	419
Db	383	AGACTTATCGATTCGACACAGTAGTTAACTGATGTGCCCTTGAGTCAATTAAACA	442
Oy	420	CGCCTTACTGCTCGCTGATTCATCCCCAGTCGCGCAGTCTATTAAGATTGAATTCAAC	479
Db	443	CGCCTTACTGCTCGCTGATTCATCCCCAGTCGCGCAGTCTATTAAGATTGAATTCAAC	502
Oy	480	CCTCCCAAACCTGTGGGCAATGATGACCTGCATCGGGAGCCTCTCATTTACGCTGAGAT	539
Db	503	CCTCCCAAACCTGTGGGCAATGATGACCTGCATCGGGAGCCTCTCATTTACGCTGAGAT	562
Oy	540	GATTAACACGAGCGGTATCAAGAGACTAAAGCTTATGGAAGACCAACAAGCAGTC	599
Db	563	GATTAACACGAGCGGTATCAAGAGACTAAAGCTTATGGAAGACCAACAAGCAGTC	622
Oy	600	CTCGNATATTTACCGAGA-AAAGAGGGTCTCTGAAACATTTCCGGAGACAGAAACCAACA	658
Db	623	CTCGNATATTTACCGAGAGAAAAGGGTCTCTGAAACATTTCCGGAGACAGAAACCAACA	682
Oy	659	GATTTGGCCCTATGATATATGCTTCTTCACAACTAAAGTCCACACAAGACCGAC- AAAG	717
Db	683	GATTTGGCCCTATGATATATGCTTCTTCACAACTAAAGTCCACACAAGACCGACAAAG	742
Oy	718	CTTCAGTT-ACTCCATGAGGAGAA-ATGTGTGTAACTTTAA	757
Db	743	CTTCAGTTAACTCCATGAGGAGAACCGGTGTGTAACTTTAA	784
RESULT 5			
BG705248			
LOCUS		706 bp mRNA linear EST 07-MAY-2001	
DEFINITION		602687928F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4820383 5',	
ACCESSION		mRNA sequence.	
VERSION		BG705248	
KEYWORDS		BG705248.1 GI:13979395	
SOURCE		EST.	
ORGANISM		human.	
REFERENCE		Homo sapiens	
AUTHORS		Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
TITLE		Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
JOURNAL		NIH-MGC http://mgc.nci.nih.gov/	
COMMENT		National Institutes of Health, Mammalian Gene Collection (MGC)	
		Unpublished (1999)	
		Contact: Robert Strausberg, Ph.D.	
		Email: cgabps@email.nih.gov	
		Source Procurement: Miklos Palkovits, M.D., Ph.D.	
		cDNA library Preparation: Michael J. Brownstein (NHGRI), Shitaki	
		Toshiyuki and Piero Carninci (RIKEN)	
		cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)	
		DNA Sequencing by: Incyte Genomics, Inc.	
		Clone distribution: MGC clone distribution information can be	
		found through the I.M.A.G.E. Consortium/LNLN at:	
		http://image.lnl.gov	
		plate: LLM10725 row: g column: 08	
		High quality sequence stop: 706.	
FEATURES		Location/Qualifiers	
source		1..706	
		/organism="Homo sapiens"	
		/db_xref="taxon:9606"	
		/clone="IMAGE:4820383"	
		/clone_id="NIH_MGC_95"	
		/tissue_type="hippocampus"	

Db 570 CCTCCCAAACTGTGGCATTGATGACTGCTGAGGAGCCCTCTCATTCAGCGTGAGAT 629
QY 540 GATTAACGAGACGGTTATCAAGAGACTAAAGCGTTATGAGACCAAAAGNAGTC 599
Db 630 GATTAACGAGACGGTTATCAAGAGACTAAAGCGTTATGAGACCAAAAGNAGTC 669
QY 600 CTGGNATATTACAGAAAAAGGGGTCTGGAACATCTCCGGAACAGAACCAACAG 659
Db 690 CTGGAATATTACAGAAAAAGGGGTCTGGAACATCTCTCGG - ACAGAACCAACAG 748
QY 660 ATTGGCCCTATGATATGCTTCTTCCACAACTAAAGTTCCAGAACGCGAAGCT 719
Db 749 ATTGG - CCTATGATATCTCTTCTTCCACAACTAAAGTTCCAGAACGCGAAGCT 807
QY 720 TCAGTACTTCATGAGAG- - - - - AATGTGTGTAATTAAT 758
Db 808 TTAAGTTACTTCATGAGAGAAATGTGTGTAATTAAT 850

RESULT 7
AV704895 716 bp mRNA linear EST 09-OCT-2000
LOCUS AV704895 ADB Homo sapiens cDNA clone ADBXH03 5', mRNA sequence.
DEFINITION AV704895.1 GI:10722206
VERSION AV704895.1 GI:10722206
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 716)
AUTHORS Peng, Y., Song, H., Huang, Q., Huang, C., Gu, Y., Yang, Y., Gao, G., Xiao
H., Xu, X., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z.,
Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu
G., Hu, R., Chen, J., Chen, Z., and Han, Z.
Homo sapiens cDNA ADB clones
Unpublished (2000)
CONTACT: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203 P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source location/Qualifiers
1..716
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ADBXH03"
/clone_lib="ADB"
/tissue_type="Adrenal gland"
/dev_stage="Adult"
/lab_host="SOLR"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 210 a 168 c 161 g 171 t 6 others
ORIGIN

Query Match 74.6%; Score 637.2; DB 10; Length 716;
Best Local Similarity 96.4%; Pred. No. 36-170;
Matches 690; Conservative 0; Mismatches 21; Indels 5; Gaps 4;

QY 126 CGCATCATACACACTTCAGCTGAAGACCTCTCCAGGGGAGCCTGCGGGGACAC 185
Db 1 CGCATCATACACACTTCAGCTGAAGACCTCTCCAGGGGAGCCTGCGGGGACAC 60

QY 186 ATGCTGCGGGGACACAGAAATTTGGCGTTAGCCAAAGCTTTTATGACCAAGGAAGTC 245
Db 61 ATGCTGCGGGGACACAGAAATTTGGCGTTAGCCAAAGCTTTTATGACCAAGGAAGTC 120

QY 246 ATCCCAAGATGATGATGACTGCGGCTGCGCTTCATGAGCTGAAAAATTCACCCAGTAT 305
|||||

Db 121 ATCCCAAGATGATGATGACTGCGGCTGCGCTTCATGAGCTGAAAAATTCACCCAGTAT 180
QY 306 AGCTGCTGTGGATGGTTTTCCAGAGACCTCCACAGGACAGAACCCAGATAGAGCT 365
Db 181 AGCTGCTGTGGATGGTTTTCCAGAGACCTCCACAGGACAGAACCCAGATAGAGCT 240
QY 366 TATCAGATGACACAGATGATTAACCTGAATGTCCTTTGAGGCTCATTTAAACACCTT 425
Db 241 TATCAGATGACACAGATGATTAACCTGAATGTCCTTTGAGGCTCATTTAAACACCTT 300
QY 426 ACTGCTGCTGGATTTATCCCGCACTGGCCAGCTATTAACATTTAAACCTCC 485
Db 301 ACTGCTGCTGGATTTATCCCGCACTGGCCAGCTATTAACATTTAAACCTCC 360
QY 486 AAACAGTGGGCGATTGATGACCTGAGGAGCCCTCATTCAGGTAGAGTGAATAA 545
Db 361 AAACAGTGGGCGATTGATGACCTGAGGAGCCCTCATTCAGGTAGAGTGAATAA 420
QY 546 CCAGAGACGGTTATCAAGAGACTAAAGCGTTATGAGACCAAAAGNAGTCGTGNA 605
Db 421 CCAGAGACGGTTATCAAGAGACTAAAGCGTTATGAGACCAAAAGNAGTCGTGNA 480
QY 606 TATTACCAGAAAAAGGGGTCTGGAACATTTCTCCGAAACAGAACCAAGATTTGG 665
Db 481 TATTACCAGAAAAAGGGGTCTGGAACATTTCTCCGAAACAGAACCAAGATTTGG 540
QY 666 CCTATGATATGCTTCTTCCACAACTAAAGTCCCAAAAG - - - - - AAGCCAAAGATTTGG 723
Db 541 CCTATGATATGCTTCTTCCACAACTAAAGTTCACAAAGGACCAAGGACCTTCAG 600
QY 724 TTATCTCATGAGG - AGAATGTGTGTA - CTATTAATAGTAGAGTGGCAACCTCTGAG 781
Db 601 NTACTTCATGAGNAAAGATGTGTATACCTATTATAGTAGATGTGGCANNCCCTGAG 660
QY 782 TCTTTCATTTAGAGCTGCTTTCT - AAGACTTGTAGTAGATGATTTCTTG 836
Db 661 GCCTTTGCTTAGAAGCTGCTTTTCTTAAAGACTTCTAGATGATGATTTCTTG 716

RESULT 8
BG106150 1183 bp mRNA linear EST 30-JAN-2001
LOCUS BG106150 602289978F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:4385034 5',
DEFINITION mRNA sequence.
ACCESSION BG106150
VERSION BG106150.1 GI:12599996
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1183)
AUTHORS NIH-MGC <http://mgi.mcl.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
COMMENT Email: cgabs-remail.nih.gov
Tissue Procurement: Louis Staudt, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LHAM10065 row: k column: 19
High quality sequence stop: 683.
location/Qualifiers
1..1183
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/clone="IMAGE:4385034"
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/tissue_type="lymphoma, cell line"

/lab_host="DH10B (phage-resistant)"
/note="Organ: Lymph. Vector: PCMV-SpOrf6; Site.1: NotI;
Site.2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH-MGC Library."

BASE COUNT 345 a 273 c 334 g 231 t

Query Match 74.4%; Score 635.4; DB 12; Length 1183;
Best Local Similarity 94.3%; Pred. No. 1.2e-169;
Matches 679; Conservative 0; Mismatches 39; Indels 2; Gaps 2;

1 GCCAGGCCCAAGCCCTGATACCCGGCGGGTGG-6GGGCTCAGTCTGGGCGATGGGGGG 59
6 GGGCAGGCCCAAGCCCTGATACCCGGCGGGTGGGCGCTCAGTCTGGGCGATGGGGGG 65
60 TCCGCGCGGCTGCTGCGAGCGGTGATCATGGGGCCCCGGGCTCGGCAAGGGCAGCGT 119
66 TCCGCGCGGCTGCTGCGAGCGGTGATCATGGGGCCCCGGGCTCGGCAAGGGCAGCGT 125
120 TCGTTCGGGCTACACTACACCTTCGAGCTAAGCAGCTCTTCACGGGGGACCTGCTCCG 179
126 TCGTTCGGGCTACACTACACCTTCGAGCTAAGCAGCTCTTCACGGGGGACCTGCTCCG 185
180 GACACATGCTGCGGGGACAGAAATGGGCTGTAGCCAAAGGCTTCATTGACCAAGG 239
186 GACACATGCTGCGGGGACAGAAATGGGCTGTAGCCAAAGGCTTCATTGACCAAGG 245
240 AAATCATCCCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 299
246 AAATCATCCCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 305
300 CAGTATAGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 359
306 CAGTATAGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 365
360 AGAGCTTATCAGATCGACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 419
366 AGAGCTTATCAGATCGACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 425
420 CGGCTTACTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 479
426 CGGCTTACTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 485
480 CCGTCCCAAACTGTGGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 539
486 CCGTCCCAAACTGTGGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 545
540 GATTAACCAAGAGCGGTTATCAAGAGCTAAAGGCTATGAAGCC-AAACAAAGNAGT 598
546 GATTAACCAAGAGCGGTTATCAAGAGCTAAAGGCTATGAAGCCAAACAAAGCCAGT 605
599 CCGTGNATATTACAGAAAAAGGGGTGCTGAACATCTCCGGAACAGAAACCAACAA 658
606 CCGTGNATATTACAGAAAAAGGGGTGCTGAACATCTCCGGAACAGAAACCAACAA 665
659 GATTGGCCCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 718
666 GATTGGCCCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 725

RESULT 9
BQ435142 924 bp mRNA linear EST 24-MAY-2002
LOCUS BQ435142
DEFINITION AGENCOURT_7914060 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:6156916
5', mRNA sequence.
ACCESSION BQ435142
VERSION BQ435142.1 GI:21174218
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 924)
AUTHORS NIH-MGC. <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: LLM13501 row: p column: 05
High quality sequence start: 225
High quality sequence stop: 379.
Location/Qualifiers

FEATURES

1. 924
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="6156916"
/clone_lib="NIH_MGC_71"
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/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: PCMV-SpOrf6; Site.1: NotI;
Site.2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb."
BASE COUNT 280 a 191 c 213 g 239 t 1 others

Query Match 74.2%; Score 633.8; DB 14; Length 924;
Best Local Similarity 97.9%; Pred. No. 3.1e-169;
Matches 641; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

200 AGAATTTGGCGTGTATGACCAAGGCTTCATTGACCAAGGCAAACTCCAGATGATGT 259
31 AGAATTTGGCGTGTATGACCAAGGCTTCATTGACCAAGGCAAACTCCAGATGATGT 90
260 CAGTACTGCGGCTGCGCTTCATGAGCTGAAAAATTCACCCAGATAGCTGGTGGGA 319
91 CAGTACTGCGGCTGCGCTTCATGAGCTGAAAAATTCACCCAGATAGCTGGTGGGA 150
320 TCGTTTCCAAAGACACTTCCACAGGCAAGCCCTGATAGACTTATCAGATCGACAC 379
151 TCGTTTCCAAAGACACTTCCACAGGCAAGCCCTGATAGACTTATCAGATCGACAC 210
380 AGTATTAACCTGAATGTCCTTTGAGGTGATTAACCAAGCCCTTACTGCTGCTGAT 439
211 AGTATTAACCTGAATGTCCTTTGAGGTGATTAACCAAGCCCTTACTGCTGCTGAT 270
91 CAGTACTGCGGCTGCGCTTCATGAGCTGAAAAATTCACCCAGATAGCTGGTGGGA 150
320 TCGTTTCCAAAGACACTTCCACAGGCAAGCCCTGATAGACTTATCAGATCGACAC 379
151 TCGTTTCCAAAGACACTTCCACAGGCAAGCCCTGATAGACTTATCAGATCGACAC 210
440 TCAATCCGCGAGTGGCGAGTCTATTAACATTTGAATTCACCCCTCCAAACTGTGGCAT 499
211 AGTATTAACCTGAATGTCCTTTGAGGTGATTAACCAAGCCCTTACTGCTGCTGAT 439
271 TCAATCCGCGAGTGGCGAGTCTATTAACATTTGAATTCACCCCTCCAAACTGTGGCAT 330
500 TGATGACCTGACCTGGGAGGCTCTCATTCACCGTGAAGATGATTAACCAAGAGGCTTAT 559
331 TGATGACCTGACCTGGGAGGCTCTCATTCACCGTGAAGATGATTAACCAAGAGGCTTAT 390
560 CAAGAGCTAAAGGCTTATGAAGACCAAAACAGNCAGTCTGAGATATTACAGAAAAA 619
391 CAAGAGCTAAAGGCTTATGAAGACCAAAACAGNCAGTCTGAGATATTACAGAAAAA 450
620 AGGGGTGCTGGAACATTTCCGGAACAGAAACCAAGATTTGGCCCTATGATATGC 679
451 AGGGGTGCTGGAACATTTCCGGAACAGAAACCAAGATTTGGCCCTATGATATGC 510
680 TTTCTCAAACTTAAAGTTCCACAAAGAGCCAGAAAGCTTCACTACTCATAGAGAGA 739
511 TTTCTCAAACTTAAAGTTCCACAAAGAGCCAGAAAGCTTCACTACTCATAGAGAGA 570
740 AATGTGTAACTTAAATGATAGATGGGCAAGCTCTAGTCTTGCATTGAAAGCT 799

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Db      571 AATGCTGAGACTATTAAATAGTAGATGGCAAACTCCTAGTCTTGATTTAGAGCT 630
QY      800 GCTTTCTAGACTCTAGTATGTATGAATCTTTGAAAATATATATCTTTTA 854
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Db      631 GCTTTTCTAGACTCTAGTATGTATGAATCTTTGAAAATATATATCTTTTA 685

RESULT 10
BI553912          833 bp  mRNA      linear  EST 05-sep-2001
LOCUS      6031908777P1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5262066 5',
DEFINITION mRNA sequence.
ACCESSION  BI553912
VERSION     BI553912.1 GI:15441224
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 833)
AUTHORS   NIH-MGC http://mgc.ncl.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
            cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki
            Toshituki and Piero Carninci (RIKEN)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLM11660 row: j column: 19
            High quality sequence stop: 801.

FEATURES
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    /clone_lib="NIH_MGC_95"
    /tissue_type="hippocampus"
    /lab_host="DH10B"
    /note="Organ: Brain; Vector: pBluescriptR (modified
    pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
    ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTNN-3',
    size-selected for average insert size 2.5 kb and
    normalized to R0T 5. This is a primary library enriched
    for full-length clones and constructed using the
    Cap-trapper method (Carninci, in preparation). Library
    constructed by M. Brownstein (NHGRI/NHGRI, National
    Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT  207 a 230 c 233 g 163 t
ORIGIN
Query Match      73.3%; Score 625.8; DB 13; Length 833;
Best Local Similarity 95.9%; Pred. No. 5,6e-167;
Matches 683; Conservative 0; Mismatches 25; Indels 4; Gaps 4;
QY      1 GCCANCCCAAGCCCTGTACCCCGCGGTG-GGGCTCACTTCGGCCATGGGGCG 59
        | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      95 GGCAGGCGCAAGCCCTGTACCCCGCGGTGCGGCCCTCACTTCGGCCATGGGGCG 154
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      60 TCCGCGCGCTGCTGCGAGCGGTGATCATGGGGCCCGGCTCGGCAAGGCAACCGT 119
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      155 TCCGCGCGCTGCTGCGAGCGGTGATCATGGGGCCCGGCTCGGCAAGGCAACCGT 214
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      120 TCGTCGCGCATCACTACACTTCGAGCTGAAGCAACCTCTCCAGCGGGACCTGCTCCG 179
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      215 TCGTCGCGCATCACTACACTTCGAGCTGAAGCAACCTCTCCAGCGGGACCTGCTCCG 274
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      180 GACAACTGCTGCGGGGCAAGAAATTTGGCTTATGCAAGGCTTTATTACCAAGGG 239
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db      275 GACAACTGCTGCGGGGCAAGAAATTTGGCTTATGCAAGGCTTTATTACCAAGGG 334
QY      240 AACATCATCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 299
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      335 AACATCATCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 394
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      300 CAGTATAGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 359
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      395 CAGTATAGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 454
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      360 AGAGCTTATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 419
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      455 AGAGCTTATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 514
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      420 CGCTTACTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 479
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      515 CGCTTACTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 574
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      480 CCTCCCAAACTGTGGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 539
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      575 CCTCCCAAACTGTGGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 634
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      540 GATTAACCGAGACGCTTATCAAGAGAC-TAAAGCTTATGAAGA-CCAAACAAGNCAG 597
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      635 GATTAACCGAGACGCTTATCAAGAGACTTAAAGGCTTATGAAGACCCAAAGCCAG 694
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      598 TCGTGNATATATACAG-AAAAAGGGGCTGGAAGACTTCCGGAACAGAAACCAAC 656
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Db      695 TCGTGNATATATACAG-AAAAAGGGGCTGGAAGACTTCCGGAACAGAAACCAAC 754
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QY      657 AAGATTGGCCCTATGATATATGCTTCTCAAACTTAAAGTTCCAAAGAA 708
        | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      755 AAGATTGGCCCTATGATATATGCTTCTCAAACTTAAAGTTCCCAAGAA 806
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 11
BI619950          902 bp  mRNA      linear  EST 18-Apr-2001
LOCUS      602618148P1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4731898 5',
DEFINITION mRNA sequence.
ACCESSION  BI619950
VERSION     BI619950.1 GI:13671321
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 902)
AUTHORS   NIH-MGC http://mgc.ncl.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLM1590 row: p column: 11
            High quality sequence stop: 772.

FEATURES
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    /db_xref="taxon:9606"
    /clone_image="4731898"
    /clone_lib="NIH_MGC_79"
    /lab_host="DH10B (TI phage-resistant)"
    /note="Organ: placenta; Vector: pDNR-LIB (Clontech);
    Site_1: SfiI (ggccgctggc); Site_2: SfiI (ggccatgatgac
    ); 5' and 3' adaptors were used in cloning as follows: 5'
    adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor

```

sequence: 5'-ATTCTAGAGCCGAGCGGCGGACATG-dt(30)BN-3'
(where B = A, C, G, or T). Average
insert size 1.3 kb (range 0.5-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
Library."

BASE COUNT 275 a 199 c 181 g 247 t
ORIGIN

Query Match 70.8%; Score 605; DB 12; Length 902;
Best Local Similarity 99.2%; Pred. No. 4.8e-161;
Matches 638; Conservative 0; Mismatches 2; Indels 3; Gaps 3;

OY 215 AGCCAGGCTTTCATTCAGCAAGGAAACATCCAGATGATGCTGCTGGCGC 274
|||||
Db 1 AGCCAGGCTTTCATTCAGCAAGGAAACATCCAGATGATGCTGCTGGCGC 60
OY 275 CCTTCATGAGCTGAAAATCTCACCCAGTATAGCTGGCTGTGGATGTTTCCAAAGAC 334
|||||
Db 61 CCTTCATGAGCTGAAAATCTCACCCAGTATAGCTGGCTGTGGATGTTTCCAAAGAC 120
OY 335 ACTTCCACAGGCAAGCCCTAGATAGAGCTTATCAGATGACACAGTGAATTAACCTGAA 394
|||||
Db 121 ACTTCCACAGGCAAGCCCTAGATAGAGCTTATCAGATGACACAGTGAATTAACCTGAA 180
OY 395 TGTGCCCTTTCAGCTTATTAACAAGCCCTTACTGCTGCTGATTCATCCCGCACTGG 454
|||||
Db 181 TGTGCCCTTTCAGCTTATTAACAAGCCCTTACTGCTGCTGATTCATCCCGCACTGG 240
OY 455 CCGAGCTATTAACATTCAGATTCACCCCTCCAAACCTGTGGGATGATGACCTGACTGG 514
|||||
Db 241 CCGAGCTATTAACATTCAGATTCACCCCTCCAAACCTGTGGGATGATGACCTGACTGG 300
OY 515 GGAGCCTCTCATTCAGCTGAGGATGATTAACAAGACGCTTATCAAGAGCTAAAGGC 574
|||||
Db 301 GGAGCCTCTCATTCAGCTGAGGATGATTAACAAGACGCTTATCAAGAGCTAAAGGC 360
OY 575 TTATGAAGACCAACAAGCAGTCTGCTGATTTACAG-AAAAAGGGGTGCTGAAA 633
|||||
Db 361 TTATGAAGACCAACAAGCAGTCTGCTGATTTACCAAAAAAGGGGTGCTGAAA 420
OY 634 CATTCCTCGGAACAGAACCAAGATTTGGCCCTATGATATGCTTCTCAAACTA 693
|||||
Db 421 CATTCCTCGGAACAGAACCAAGATTTGGCCCTATGATATGCTTCTCAAACTA 480
OY 694 AAGTTCACAAAGACCCAGAAAGCTTCAGTACTCCATGAGAGAAA-TGTGTGTA-C 751
|||||
Db 481 AAGTTCACAAAGACCCAGAAAGCTTCAGTACTCCATGAGAGAAA-TGTGTGTA-C 540
OY 752 TATTATAGTAAGATGGGCAAACTCCTAGTCTTGCATTTAGAGGTGCTTTTCTTAAG 811
|||||
Db 541 TATTATAGTAAGATGGGCAAACTCCTAGTCTTGCATTTAGAGGTGCTTTTCTTAAG 600
OY 812 ACTTCTAGTATGATGAATCTTTGAAAAATTATTAATCTTTA 854
|||||
Db 601 ACTTCTAGTATGATGAATCTTTGAAAAATTATTAATCTTTA 643

RESULT 12
AUI26983 639 bp mRNA linear EST 01-AUG-2002
LOCUS AUI26983
DEFINITION Homo sapiens cDNA clone NT2RP2000329 5', mRNA
sequence.
ACCESSION AUI26983
VERSION AUI26983.1 GI:10951699
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 639)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,

TITLE Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Isogai,T.
JOURNAL HRI human CDNA project
COMMENT Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human CDNA project: 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.

FEATURES
source
Location/Qualifiers
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/cell_line="NT2"
/note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor
cells after 2-weeks retinoic acid (RA) induction"

BASE COUNT 170 a 167 c 155 g 138 t 9 others
ORIGIN

Query Match 69.7%; Score 595.2; DB 9; Length 639;
Best Local Similarity 96.1%; Pred. No. 2.6e-158;
Matches 614; Conservative 0; Mismatches 24; Indels 1; Gaps 1;

OY 37 CTCAGTCTGGGCCATGAGGGGCGTCCGCGGCTGTCGACAGCGGATCATGAGGGGCC 96
|||||
Db 1 CTCAGTCTGGGCCATGAGGGGCGTCCGCGGCTGTCGACAGCGGATCATGAGGGGCC 60
OY 97 CGGGCTCGGGCAAGGGCAGCTGTCGCGGCACTACACTTGAGCTGAGAGACC 156
|||||
Db 61 CGGGCTCGGGCAAGGGCAGCTGTCGCGGCACTACACTTGAGCTGAGAGACC 120
OY 157 TCTCCAGCGGGGACCTGCTCCGGGACAACTGTCGCGGGCCACAGAAATTTGGCTGTTAG 216
|||||
Db 121 TCTCCAGCGGGGACCTGCTCCGGGACAACTGTCGCGGGCCACAGAAATTTGGCTGTTAG 180
OY 217 CCAAGCTTTCATTTAGACCAAGGAACTCATCCAGATGATGTCATGCTGCTGGCCC 276
|||||
Db 181 CCAAGCTTTCATTTAGACCAAGGAACTCATCCAGATGATGTCATGCTGCTGGCCC 240
OY 277 TTCATGAGCTGAAAATCTCACCCAGATATGAGTGGCTGTTGGATGGTTTCCAAAGCAC 336
|||||
Db 241 TTCATGAGCTGAAAATCTCACCCAGATATGAGTGGCTGTTGGATGGTTTCCAAAGCAC 300
OY 337 TTCACAGGAGAAAGCCCTAGATAGAGCTTATCAGATGACACAGTGAATTAACCTGAATG 396
|||||
Db 301 TTCACAGGAGAAAGCCCTAGATAGAGCTTATCAGATGACACAGTGAATTAACCTGAATG 360
OY 397 TGGCCTTTGAGGTCATTAACAACGCTTACTGCTCCCTGATTCATCCCGCAGTGGCC 456
|||||
Db 361 TGGCCTTTGAGGTCATTAACAACGCTTACTGCTCCCTGATTCATCCCGCAGTGGCC 420
OY 457 GAGCTATTAACATTTGAATTCACCCCTCCAAACCTGTGGGATGATGAGCTGACTGGGG 516
|||||
Db 421 GAATCTATTAACATTTGAATTCACCCCTCCAAACCTGTGGGATGATGAGCTGACTGGGG 480
OY 517 AGCCTTCATTCAGCGTGAAGATGATTAACACAGAGAGCTTATCAAGAGCTTAAGGCTT 576
|||||
Db 481 A-CCTTCATTCANCGTGAAGATGATTAACACAGAAACNGTTATCAAGAACTAAAGCTT 539
OY 577 ATGAAGACCAACAAGNCAGTCTGSGNATATTAACGAAAAAGGGGTGCTGGAACAT 636
|||||
Db 540 ATGAAGACCAACAAGNCAGTCTGSGNATATTAACGAAAAAGGGGTGCTGGAACAT 599
OY 637 TCTCCGAGACAGAAACCAAGATTTGGCCCTATGAT 675

Db	600	TCTCCGGAACANAACCAACANATTGGNCTATTTT	638
RESULT_13			
LOCUS	AV695155	716 bp	mRNA
DEFINITION	AV695155 GKC Homo sapiens CDNA clone GKCASP12 5'		linear
ACCESSION	AV695155		EST 16-JAN-2002
VERSION	AV695155.1	GI:10297018	mRNA sequence.
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 716)		
	Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z., and Han,Z.		
	Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver		
	Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)		
	21625106		
JOURNAL	Contact: Zequang Han		
MEDLINE	Chinese National Human Genome Center at Shanghai		
COMMENT	351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China		
	Tel: 86-21-50801919(ex.45)		
	Fax: 86-21-50801922		
	Email: hanzq@chgc.sh.cn		
	This clone is available at CHGC in Shanghai.		
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	/lab_host="SOLR"		
	/note="Vector: pbluescript sk(-); Site_1: EcoRI; Site_2: XhoI"		
BASE COUNT	179 a 190 c 199 g 145 t	3 others	
ORIGIN			
Query Match	69.6%; Score 594.2; DB 10; Length 716;		
Best Local Similarity	98.4%; Pred. No. 5.2e-158;		
Matches 607; Conservative %	0; Mismatches 9; Indels 1; Gaps 1;		
QY	1 GCCANAGCCCAAGCCCTGGTACCCGGCGGGG-GGGCTCAGTGTGGCGCCATGGGGCG	59	
Db	9 GGCAGGCGCAAGCCCTGGTACCCGGCGGGGCTCAGTGTGGCGCCATGGGGCG	68	
QY	60 TCCGCGGGGCTGTGCGAGCGGGTATCATGGGGGCCCGGCGCTGGGGCAAGGCAACCGT	119	
Db	69 TCCGGGGGGCTGTGCGAGCGGGTATCATGGGGGCCCGGCGCTGGGGCAAGGCAACCGT	128	
QY	120 TCGTGGCGCATCTACACACTTGAAGTGAAGCACTCTTCACGGGGGACCTGCTCCG	179	
Db	129 TCGTGGCGCATCTACACACTTGAAGTGAAGCACTCTTCACGGGGGACCTGCTCCG	188	
QY	180 GACAAACATGCTGGGGGACAGAAATGGCGTGTATGCAAGGCTTTCATTGACCAAGG	239	
Db	189 GACAAACATGCTGGGGGACAGAAATGGCGTGTATGCAAGGCTTTCATTGACCAAGG	248	
QY	240 AAATCATCCAGATGATGTTCATGACTCGGCTGGCCCTTCATGAGCTGAAAAATCTCAC	299	
Db	249 AAATCATCCAGATGATGTTCATGACTCGGCTGGCCCTTCATGAGCTGAAAAATCTCAC	308	
QY	300 CAGTATAGCTGGCTGTGGATGATGTTTTCAGAGCACTTCACAGGAGAAAGCCCTAGAT	359	

Db	309	CAGTATAGCTGGGCTGTTGGATGGTTTTTCCAGAGACACTTCCACAGCAGACAGACAGCCCTAGAT	368
QY	360	AGAGCTTATCAGATTCGACACACAGTGTATTAACCTGAAATGTCCCTTTGAGGTCAATTAAACA	419
Db	369	AGAGCTTATCAGATTCGACACACAGTGTATTAACCTGAAATGTCCCTTTGAGGTCAATTAAACA	428
QY	420	CGGCTTACGCTGCTGGGATTCATCCCGGACAGGCGCGAGTCTATTAACATTGAATTCAAC	479
Db	429	CGGCTTACGCTGCTGGGATTCATCCCGGACAGGCGCGAGTCTATTAACATTGAATTCAAC	488
QY	480	CTCCCAAAACCTGTGGGCATTTGATGACCTGACTGGGAGCCCTTCATTCAGCGTAGAGAT	539
Db	489	CTCCCAAAACCTGTGGGCATTTGATGACCTGACTGGGAGCCCTTCATTCAGCGTAGAGAT	548
QY	540	GATTAACCGAGAGCGGTTTTCAGAGACATTAAGGCGTTATGAAGACCAACAAGACAGC	599
Db	549	GATTAACCGAGAGCGGTTTTCAGAGACATTAAGGCGTTATGAAGACCAACAAGACAGC	608
QY	600	CTGGNATATTACAGAA	616
Db	609	CTGGNATATTACAGAA	625
RESULT 14			
BG687423		711 bp	mRNA
LOCUS			linear
DEFINITION	BG687423	602639584F1 NIH_MGC_59	Homo sapiens cDNA clone IMAGE:4762436 5',
ACCESSION	BG687423		mRNA sequence.
VERSION	BG687423.1	GI:13918820	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 711)		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/.		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-r@mail.nih.gov		
	Tissue Procurement: ATCC		
	cDNA Library Preparation: CLONTECH Laboratories, Inc.		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNLN at:		
	http://image.llnl.gov		
	Plate: IlcM1616 row: h column: 21		
	High quality sequence stop: 704.		
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	/lab_host="DH10B (TI phage-resistant)"		
	/note="Organ: Lung; Vector: pDNR-LIB (Clontech); Site_1:		
	SfiI (ggcgccgcgcgc); Site_2: SfiI (ggccataggcc);		
	Double-stranded cDNA was prepared from cell line RNA. 5'		
	and 3' adaptors were used in cloning as follows: 5'		
	adaptor sequence: 5'-CACGGCATTAATGCGC-3' and 3' adaptor		
	sequence: 5'-ATTCTAGAGCCGAGCGCGCGACATG-dt(30)BN-3'.		
	(where B = A, C, or G and N = A, C, G, or T). Average		
	insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies		
	contained inserts by PCR. This library was enriched for		
	full-length clones and was constructed by Clontech		
	Laboratories (Palo Alto, CA). Note: this is a NIH-MGC		
	library."		
BASE COUNT	220 a 152 c 148 g 191 t		
ORIGIN			

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GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: March 19, 2003, 04:25:24 ; Search time 80 Seconds
(without alignments)
3273.774 Million cell updates/sec

Title: US-10-006-190-2

Perfect score: 854
Sequence: 1 GCCAGCCCAAGCCCTGCT.....TCGAATATATATTACTTTTA 854

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents.NA.*

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5: /cgn2_6/ptodata/1/ina/PCRTS.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/Backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	851	99.6	854	2	US-08-829-027-2
2	851	99.6	854	3	US-09-225-366-2
3	835.2	97.8	1751	4	US-09-149-476-68
4	81.2	9.5	669	4	US-09-134-001C-452
5	62	7.3	11831	4	US-08-961-527-65
6	40	4.7	30001	1	US-08-125-468-1
7	40	4.7	30001	2	US-08-474-933-1
8	38.8	4.5	10095	3	US-08-822-586-45
9	38.4	4.5	4530	4	US-09-221-017B-913
10	37.8	4.4	3001	4	US-09-387-212-9
11	37.8	4.4	3001	4	US-09-848-802-9
12	37.2	4.4	7218	1	US-08-232-463-14
13	36.8	4.3	3472	6	5244792-1
14	36	4.2	9960	3	US-08-822-586-46
15	35.2	4.1	2098	4	US-09-257-541-3
16	35.2	4.1	28882	4	US-08-961-527-140
17	33.8	4.0	388	1	US-07-626-618A-1
18	33.8	4.0	388	1	US-07-928-611-1
19	33.8	4.0	388	2	US-08-333-977-1
20	33.8	4.0	388	2	US-08-487-811A-1
21	33.8	4.0	388	4	US-09-060-694-1
22	33.8	4.0	388	4	US-09-378-074-1
23	33.8	4.0	388	5	PCT-US93-07370-1
24	33.8	4.0	530	3	US-08-758-662-4
25	33.8	4.0	1370	3	US-08-475-742-3
26	33.8	4.0	1370	1	US-08-056-051-1
27	33.8	4.0	1370	1	US-07-928-611-17

28	33.8	4.0	1370	2	US-08-487-811A-17	Sequence 17, Appl
29	33.8	4.0	1370	4	US-09-060-694-17	Sequence 17, Appl
30	33.8	4.0	1370	4	US-09-378-074-17	Sequence 17, Appl
31	33.8	4.0	1370	5	PCT-US93-07370-17	Sequence 3, Appl
32	33.8	4.0	1466	1	US-08-056-051-3	Sequence 19, Appl
33	33.8	4.0	1466	1	US-07-928-611-19	Sequence 19, Appl
34	33.8	4.0	1466	2	US-08-487-811A-19	Sequence 19, Appl
35	33.8	4.0	1466	4	US-09-060-694-19	Sequence 19, Appl
36	33.8	4.0	1466	4	US-09-378-074-19	Sequence 5, Appl
37	33.8	4.0	1466	5	PCT-US93-07370-19	Sequence 21, Appl
38	33.8	4.0	1610	1	US-08-056-051-5	Sequence 21, Appl
39	33.8	4.0	1610	1	US-07-928-611-21	Sequence 21, Appl
40	33.8	4.0	1610	2	US-08-487-811A-21	Sequence 21, Appl
41	33.8	4.0	1610	4	US-09-060-694-21	Sequence 21, Appl
42	33.8	4.0	1610	4	US-09-378-074-21	Sequence 21, Appl
43	33.8	4.0	1610	5	PCT-US93-07370-21	Sequence 7, Appl
44	33.8	4.0	4524	2	US-08-845-998-7	Sequence 7, Appl
45	33.8	4.0	4524	3	US-09-206-537-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-08-829-027-2
Sequence 2, Application US/08829027
Patent No. 5856160
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/829,027
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0256 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 854 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Consensus
CLONE: 2122022
US-08-829-027-2
Query Match 99.6%; Score 851; DB 2; Length 854;
Best Local Similarity 100.0%; Pred. No. 2.3e+248;
Matches 854; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

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US-09-225-366-2
; Sequence 2, Application US/09225366
; Patent No. 6001624
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.

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? STREET: 3174 Porter Drive
? CITY: Palo Alto
? STATE: CA
? COUNTRY: USA
? ZIP: 94304
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FastSeq for Windows Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/225.366
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/829,027
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Billings, Lucy J.
? REGISTRATION NUMBER: 36,749
? REFERENCE/DOCKET NUMBER: PF-0256 US
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415-855-0555
? TELEFAX: 415-845-4166
? TELEX:
? INFORMATION FOR SEQ ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 854 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? IMMEDIATE SOURCE:
? LIBRARY: Consensus
? CLONE: 2122022
? US-09-225-366-2

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Query Match          99.6%; Score 851; DB 3; Length 854;
Best Local Similarity 100.0%; Pred. No. 2,3e-248;
Matches 854; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GCCANGCCCAAAAGCCCTGTACCCGCGGTGGGGCCTCAGTCTGCGCCATGGGGCGT 60
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Db 61 CCGCGGCGCTGCTGCGAGCGGTGATCATGGGGCCCCGGGCTCGGGCAAGGCGACCTGT 120
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Db 361 GAGCTTATCAGATCGACACAGTATTAACCTGATGCTTTGAGTCAATTAACCAAC 420
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Db 841 TTATATTACTTTTA 854
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US-09-149-476-68
; Sequence 68, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; EARLIER FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02

Query Match 97.8%; Score 835.2; DB 4; Length 1751;
Best Local Similarity 99.2%; Pred. No. 2,1e+243;
Matches 848; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1 GCCAAGCCCAAGCCCTGCTACCCGCGGCTG-6GGCTCAGCTTCGGCCATGGGGCG 59
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QY 60 TCCGGCGGCTGCTGCGAGCGGTGATGAGGCGCCCGCGCTCGGCAAGGCGACCCGTG 119
DB 104 TCCGGCGGCTGCTGCGAGCGGTGATGAGGCGCCCGCGCTCGGCAAGGCGACCCGTG 163
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QY 420 CCGCTTACTGCTGCGTGATTCATCCCGCCAGTGGCGGAGTATTAACCTTAATTTCAAC 479
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RESULT 8

US-08-822-586-45
; Sequence 45, Application US/08822586
; Patent No. 6015890

GENERAL INFORMATION:

APPLICANT: WILLIAM R. JACOBS, JR., JAMES M. MUSSER AND
APPLICANT: AMALIO TELENTE
TITLE OF INVENTION: AN EMBCAB OPERON OF MYCOBACTERIA AND
TITLE OF INVENTION: MUTANTS THEREOF
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESS: AMSTER, ROTHSTEIN & EBENSTEIN
STREET: 90 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.

ZIP: 10016

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH 1.44 MB STORAGE
MEDIUM TYPE: DISKETTE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,586

FILING DATE: MARCH 20, 1997

ATTORNEY/AGENT INFORMATION:
NAME: ELIZABETH A. BOGOSIAN

REGISTRATION NUMBER: 39,911

REFERENCE/DOCKET NUMBER: 96700/437

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-5995

TELEFAX: (212) 286-0854 or 286-0082

TELEX: TWX 710-581-4766

INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:

LENGTH: 10095
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO

US-08-822-586-45

Query Match 4.5%; Score 38.8; DB 3; Length 10095;
Best Local Similarity 51.1%; Pred. No. 0.19; Mismatches 87; Indels 0; Gaps 0;

Matches 91; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

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DB 4854 GCCGGGCGACCGATGACGTGCGCGCGGTGGCGGTGCGTGGCGGGCGTTCGCTGA 4913

QY 73 TCGGACGGTGCATGAGGGGCGCGGCTCGGGCAAGGGCAGCGTGTGCTCGCGCATCA 132

DB 4914 TACCGTGTGGTGTTCGGGACCAACGCTGCGCACGGTGGCGCGATCGGACGATCA 4973

QY 133 CTACACACTTCAGTGAAGACCTCTCCAGCGGGAGCTGCTCGGGACACATGCT 190

DB 4974 AGTACAAGTGGCGCCGACCATGCTGTGACAGAGACTTCTGCGCTACTTCTCT 5031

RESULT 9

US-09-221-017B-913
; Sequence 913, Application US/09221017B
; Patent No. 6444789

GENERAL INFORMATION:

APPLICANT: ROSS, BRUCE C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF

NUMBER OF SEQUENCES: 1120

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FORSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows

SOFTWARE: FASTSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B

FILING DATE: 23-DEC-1998

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182

FILING DATE: 31-DEC-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1546

FILING DATE: 30-JAN-1998

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911

FILING DATE: 09-APR-1998

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023

FILING DATE: 10-DEC-1998

ATTORNEY/AGENT INFORMATION:
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TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 913:

SEQUENCE CHARACTERISTICS:

LENGTH: 4530 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: UNKNOWN

ORIGINAL SOURCE:
ORGANISM: PORPHYROMONAS GINGIVALIS

FEATURE:
NAME/KEY: misc.feature

LOCATION: 1...4530

US-09-221-017B-913

Query Match 4.5%; Score 38.4; DB 4; Length 4530;
Best Local Similarity 48.0%; Pred. No. 0.16;

Matches 142; Conservative 0; Mismatches 151; Indels 3; Gaps 1;

QY 68 GCTGCTCGAGCGGTGATCATGGGGGCGCGGCTGGGGCAAGGGCAGCTGTGTCGG 127

DB 4131 GATGCTTAACGTAATCTTCGCTGCTCCGCTTCGCGGAAGGGCCCAAGCGAAGA 4190

QY 128 CATCAGTACAGCTGTGAGTGAAGACCTCTCAGCGGGGAGCTGCTCGGGACAACAT 187

DB 4191 ACTGATCCGTCGATATGATTCGCGCATATTTCAACCGAGAGTGTGTCGCCAAT 4250

QY 188 GCTCGGGGACAGAAATTCGCTGTAGCCAAAGCTTTTATTTGACCAAGCAATCAT 247

DB 4251 CAAAGCTCAGACCGAAGTGGCGCAAGCAGCGCGCTATCATCAAGAGGACACCTCGT 4310

QY 248 CCGAGATGATGATGATGCTGGCGCTTCATGAGCTGAAAAATTCACCA---GTA 304

DB 4311 ACCTGACAGCGTATGCTGTGATGATGAAAAAGCTCATCAGCATTTGTCGATACCGA 4370

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